SCCCRT100 FGAS02325

Arabidops Arabidops

1007056A0

Arabidops

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SCAGFL109 FGAS02788

OGYCI 27TH

FGAS02642

Arabidops Talri176F GQ015M12. HVSMEn000

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EBes01 SQ OGWIF61TV 1123005E0

Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Minimum DB E Maximum DB E

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960 bp DNA linear GSS 16-MAY-2003 OGIAQ20TV ZM 0.7 1.5 KB Zea mays genomic clone ZMWBMa0359C15, genomic survey sequence.
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 960)

Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Praser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Consortium for Maize Genomics
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CA7109355
CC7130686
CA130686
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CC214113
CCG73495
CC347713
CCG734025
CC3470387
CCG734025
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CCG74494
BF19999708
CK214494
BH198967
BK833153
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CG240387
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Class: sheared ends.
Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cathy Whitelaw
TIGR
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CG240397 OGYCI27TV
CG453578 OGSAD40TV
CC344824 OGIAQ20TH
CC724960 OGIAB23TV
CG284572 CGWIF6ITH
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CA13480 SGJFR106
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                                                                        June 17, 2005, 03:30:48; Search time 3690 Seconds (without alignments) 2981.185 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Zea mays
Zea mayota; Viridiplantae; Streptophyta; Enloopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
Zea . (bases 1 to 923)
Zea . (base . A. Reabush, J., Van Aken, S., Utterback, T.,
Zea . (clak, R. W., Nunberg, A., Robbins, D. and Lakey, N.
Zetek, R. W., Nunberg, A., Robbins, D. and Lakey, N.
Zea . (consortium foor Maize Genomics
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methylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Zea mays
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CC344824 GI:30814230 GSS.
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSs: OGS9A040TH
Contact: Cathy Whitelaw
                                                                                 uSerginLeuArgGluLeuLysAlaTrpPheGluGluGluGlnThrLeuPheHisPheTyrSe
                                                                                                                          GCCGTCCATTCTTCTCGCCCTATGATGCTGCTGCAGTCGCAGCGCGGAGGTGGGGGGGTGG
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Zea mays c
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9712 Medical Center Drive, Rc
Tel: 301-838-584
Fax: 301-838-0208
Email: whitelaw@tigr.org
Class: sheared ends.
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CG9AA40TV ZM_0.7_1.5_KB_Zegenomic survey sequence.
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CC724960 867 bp DNA linear GSS 23-JUN-2003 CGLAB23TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0307C22, genomic survey sequence.
CC724960
CS724960.1 GI:32143893
GSS.
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1 (Bases 1 to 867)
Whitelaw, C.A., Graer, G., Wudiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Other GSSs: OGLAB23TH
Contact: Cathy Whitelaw
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                   392 GAGCAGACTCTGTTCCACTTCTACTCGGCGTCGATTCTTCTGGCCTATGATGCTGCAC
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                                                                  ValAlaAlaGlyGlyAspGlyGlyGlyValThrValLysLeuValAspPheAlaHisVal
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methylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Class: sheared ends.
Location/Qualifiers
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(bases 1 to 873)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Click, R., Nubarg, A., Robbins, D. and Lakey, N.

Unpublished (2002)
                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                  organism="Zea mays"
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Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: bloared ends.
Location/Qualifiers
1. 719
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methylation filtered genomic DNA library"
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1 (bases 1 to 719)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                           ProGlyGluProHisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaPro 100
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
                                                                                                                                                                           Contact: Cathy Whitelaw
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656 bp mRNA linear EST 25-SEP-2003 SCBGFL5081A03.g Saccharum officinarum FL5 Saccharum officinarum CDNA clone SCBGFL5081A03 5', mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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The libraries that made SUCEST
The libraries that made SUCEST
Contact: Arruda Paiol. 24 (1-4), 1-7 (2001)
Contact: Arruda Paiologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1139
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
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//clone lib="RTI"
//oce="Organ: Root tips (0.3cm-long) from adult plants;
//occa: psporti; Sitel : Salf; Site=2: NotLif, An
unidirectional cDNA library generated from [Root tips
unidirectional cDNA library generated from [Root tips
(0.3cm-long) from adult plants]. cDNA was prepared from
polyst mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
                                                                                            SCJFRT1061H11.g RT1 Saccharum Officinarum cDNA clone SCJFRT1061H11 CA134480
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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Plate: 061 row: H column: 11
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Vetrore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda, Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1187
Eax: 55 19 3788 1089
Email: parruda@unicamp.br
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Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 004 row: G column: 05
Seq primer: T7 Promoter Primer.
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Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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/db_xref="taxon:4547"
/clone="SCCCRT1004G05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGTCCGCTCATCGACGGCTCTGGCCTCTTCTACAAGCCGCTCCAGGTCGGGACCGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 ATCCGGGACACCTTCTTCCCGCGGTTTCACGGCACGCGACCCTCCCCCACCGAGGGGGGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysvalalaaspileLysileGlyalaileThrTrpProProSerSerProGluProTyr 120
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/db_xref="taxon:4547"
/clone="SCBGFL5081A03"
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                                           Seg primer: T7 Promoter Primer Location/Qualifiers
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/lab_host="adult".
/lab_host="DHIOB"
/clone lib="1123 - RescueMu Grid L"
/clone lib="1123 - RescueMu Grid L"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BgJII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb iastate.edu' and follow the links for 'RescueMu.' Grid Lwas grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BgIII, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA202412 671 bp mRNA linear EST 25-SEP-2003 SCREFL1009H02.g FL1 Saccharum officinarum cDNA clone SCRLFL1009H02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCGTCGCAGACATCAAGATCGGCGCCATCACGTGGCCACCGAGTTCGCCGGAGCCCTAC 387
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99.47%
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clade; Panicoideae; Andropogoneae; Zea.
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                   SerGlyValArgValValGlyProGluGlyAlaValTrpArgThrGluArgProGluVal
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Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotostenford.edu
Plate: 1123005
Column: 3
Class: transposon-tagged.
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Submitted (15-ARR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZMDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.radb.isatate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.isatate.edu.

Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 3374)

Hainey,C.F., Dolan, M., Morgante, M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes

Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                  161 LysAlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSerValAla
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//lab host="DHIOB"
//lab host="Organ: Inflorescence at begining of development
//localing); Vector: pSport1; Site 1: Sal1; Site 2: Not1;
An unidirectional cDNA library generated from
[Inflorescence at begining of development (Icm-long)].
cDNA was prepared from poly4+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-28 40cm-columns and
fragments sizing between 0,8 and 1.5 KD were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
                                                                  Saccharum officinarum
Bukaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheophyta,
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Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1189
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 009 row: H column: 02
Seq primer: T7 Promoter Primer.
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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722 bp DNA linear GSS 23-JUN-2003 GGLAB22TH ZM 0.7_1.5_KB Zea mays genomic clone ZNMBMa0307C22, GC724950 GC724950.1 GI:32143883 GSS GC724950.1 GI:32143883
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1 (Dases 1 to 72)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Other GSSs: OGIAB23TV
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 ValGlyProGluGlyAlaValTrpArgThrGluArgProGluValLysAlaMetAspThr 165
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/clone="zwmBMA0307C22"
/clone lib="zw 0.7.1.5 KB"
methylation filtered genomic DNA library"
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Gaps:
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                                                                                                                                                                                                                                                                                                            Tel: 301-838-5843
Fax: 301-838-5843
Fax: 301-838-0208
Fax: 301-838-0208
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 72
/ Corganism="Zea mays"
/ mol_type="genomic DNA"
/ strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-042-894A-8 (1-289) x CC724950 (1-722)
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Triticum aestivum (bread wheat)
Triticum aestivum (bread sheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://sucest.lad.ic.unicamp.br/public'
                                                                   744
191
12
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                                                                 Length:
Matches:
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FGASO23256 Triticum aestivum FGAS:
aestivum cDNA, mRNA sequence.
CK211413
EX11413.1 GI:39617517
                                                                                                                                                        Gaps:
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5', mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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                                                                                                                                                                                                                                                                                         245
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                                                     357
                                                                                      225
                                                                                                                                                                                           237
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 004 row: G column: 06
Seq primer: 17 Promoter Primer.
Location/Qualifiers
                 uValAspPheAlaHisValAlaGluGlyAspGlyValIleAspHisAsnPheLeuGlyGl
                                                                                                          GCTCAAGGCGTGGTTCGAGGGCAGACTCTGTTCCACTTCTACTCGGCGTCGATTCTTCT
                                                                                                                                                          uGlyTyrAspAlaAlaAlaValAlaAlaGlyGlyAspGlyGlyValThrValLysLe
                                                                                                                                                                             GGGCTATGATGCTGCTGCAGTCGCAGCAGCGGAGGTGGGGGGTGACGTGAGGTGAGCT
                                                                                        uLeuLysAlaTrpPheGluGluGlnThrLeuPheHisPheTyrSerAlaSerIleLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The libraries 1 to 744)

Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Arruda, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Saccharum officinarum"
/mol_type="mRNA"
/mol_type="mRNA"
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/clone="SCCCRT1004G06"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone lib="RT1'
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Saccharum officinarum
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/Glone lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/Glone lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/Glone lib="Triticum aestivum FGAS: Library 6 Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstear
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20Cs from wheat cultivar Norstear after
short exposure times to low temperature in the light and
in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4C
in the light. 1cm crown sections and green leaf tissu were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. The last 6 populations: After 7
of growth at 20C, wheat plants were transferred to 4C in
the dark. 1cm crown sections and green leaf tissu were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. First strand synthesis in this
library was done in the presence of methylaced dcTP
thereby protecting from internal cleavage with Not! In
addition, this library used a primer for second strand
synthesis that annealed to an artificial sequence (RNA)
of icn addition, adach therefore when a primer for second strand
synthesis that annealed to an artificial sequence (RNA)
                                                                                                                                                                                                                                                    University of Saskatchewan, Department of Computer Science
University of Saskatchewan, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phris sequence is the direct result of the Base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [1,797].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligo) added before first strand synthesis. Therefore when sequences from BST generated from this library will be masked for vector and adaptor sequences, an additional masking srep will have to be included to mask this RNA oligo that is common to all clones (sequence
Pooldeae, Triticeae, Triticum.
1 (bases 1 to 1191)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McGarthy, B.L., Monroy, A., Muzak, I., Nilson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68002 row: B column: 15.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:4565"
                                                                                                                                                                                      Unpublished (2003)
Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the region [1,797]
Plate: L6B002 row
                                                                                                                                                                                                                                              Bioinformatics
                            REFERENCE
AUTHORS
                                                                                                                                                          TITLE
JOURNAL
COMMENT
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1191 183 18 68 4 Conservative: Mismatches: Indels: Length: Matches: Gaps: 4.11e-87 926.00 73.63% 67.03% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: .. 80 .. Score:

US-10-042-894A-8 (1-289) x CK211413 (1-1191)

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1064 CCCGGAGACCAGGTTCCCGGCCACCCGCGCCCCAGAAAGATTGGGCCCTTTGTTGAC 1005 7 ProGluHisGinValAlaGlyHisArgAlaSerAlaSerLysLeuGlyProLeuIleAsp 26 g

27 GlySerGlyLeuPheTyrLysProLeuGlnAlaGlyAspArgGlyGluHisGluValAla 46

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completed: June 17, 2005, 06:34:53 Job time : 3703 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Total number of hits satisfying chosen parameters: 12109

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	0 111111111111111111111111111111111111	1 4 4 1 4 C

## ALIGNMENTS

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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
                                                                                                                4.71e-172
1521.00
100.00$
100.00$
                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                     LENGTH: 1344
TYPE: DNA
ORGANISM: Zea mays
                                                                        , NAME/KEY: CDS
; LOCATION: (52)
US-10-042-894A-7
                                                                                                     Alignment Scores:
Pred. No .
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Sequence 3, Application US/10042894A

Sequence 3, Application US/10042894A

Publication No. US20030099011A1

GENERAL INFORMATION:
APPLICANT: Baach, Larry
APPLICANT: Baach, Larry
APPLICANT: Rafalski, Antoni J.
TITLE OF INVENTION: No. US20030009011A1el Inositol Polyphosphate Kinase
TITLE OF INVENTION: No. US20030009011A1el Inositol Polyphosphate Kinase
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR PILITED DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-425-115-74438

US-10-425-115-74438

Sequence 74438, Application US/10425115

PUBLICATION NO. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53.22)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 200-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 74438
LENGTH: 1426
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                                                                                                AspGluGlyMetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyLysGlyGlyValLeu
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    ATCGCCAAGTGCCTCGCCATGGACCGCGGGACCACGAGGGTTCTGCTCGGATTCCGCGTC
                             SerGlyValArgValValGlyProGluGlyAlaValTrpArgThrGluArgProGluVal
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ORGANISM: Zea mays
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APPLICANT: Shi, Jinrui
APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
ITILE OF INVENTION: No. US2003009011A1e1 Inositol Polyphosphate Kinase
ITILE OF INVENTION: Genes and Uses Thereof
ITILE OF INVENTION: Genes and Uses Thereof
ITILE OF INVENTION: Canonia Canonia Canonia Current APPLICATION NUMBER: US/10/042,894A
CURRENT APPLICATION NUMBER: US 60/261,465
PRIOR PELING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1169
     833 CAACTICCTGGGCGGGCTCTGCTAGCTGATCAAGTTCGTTTCTGACATTGTTCCAGAGAC 892
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                                                                                            US-10-042-894A-1; Sequence 1, Application US/10042894A; Publication No. US20030009011A1; GENERAL INFORMATION:
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (84)...(80)
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Query Match:
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Matches:
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Mismatches:
Indels:
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96.21%
95.52%
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                             TYPE: DNA
ORGANISM: Zea mays
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Best Local Similarity:
                                                                  ; NAME/KEY: CDS
; LOCATION: (53)
US-10-042-894A-3
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SEQ ID NO 3
LENGTH: 923
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WS-10-042-894A-15

Sequence 15, Application US/10042894A

Publication No. US20030009011A1

GENERAL INFORMATION:
APPLICANT: Shi, Jinrui
APPLICANT: Shi, Jinrui
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Refalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Wo. US20030009011A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/042,894A

CURRENT FILING DATE: 2002-01-09

PRIOR FILING DATE: 2001-01-12
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121 IleAlaLygCysLeuAlaLysAspArgGlyThrThrSerValLeuLeuGlyPheArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/10042894A
; Sequence 20, Application US/20030009011A1
; GENERAL INFORMATION:
    APPLICANT:
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      TTGC--GTCCGAGTCGTCGGCCCCGGAGGCCCCTGTGGCGGAGCGGAGCGCCCGGAGGTG
                                                               LysAlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSer-ValAl
                                                                                              AAGGCTATGGACACCGTCGGCGTCCGCCGGGTGCTCCGGCCTACGTGTCATCGTCTTGC
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (72)
US-10-042-894A-20
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US-10-042-894A-20
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LOCATION: (72)
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Sequence 4650, Application US/10437963
; Sequence 4650, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Eaco, Yoigwei
; APPLICANT: Cao, Yoigwei
; APPLICANT: Cao, Yoigwei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: WHORE: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; ROWNERN FILING DATE: ADMINISTRE ADMINISTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 GCCCCCTCGTCGACGCGAGGGCTCTTCTACAAGCCCCTCCAGGCCGGGGAGCGCGGG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysValAlaAspilelysileGlyAlaileThrTrpProProSerSerProGluProTyr 120
     SASDPheLeuGlyGlyLeuCysSerLeuIleLysPheValSerAspIleValProGluTh
                     TCCGACCTGCGCCCGCCGGAGCACCAGGTGGCGGGGGCACCGCCGTCCGCCGACAAGCTG
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-437-963-4650
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1148.50
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77.03%
                                                                         280 rProHisThrGln 284
                                                                                                         874 rccrragaccas 886
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                            RESULT 8
US-10-437-963-4650
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Pred. No.:
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                     4.0
                     Version
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows
SEQ ID NO 15
LENGTH: 899
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88.42%
87.02%
81.07%
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Best Local Similarity:
Query Match:
DB:
                                                                      TYPE: DNA
ORGANISM: Zea mays
                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (89)
US-10-042-894A-15
                                                                                                                                                                                            Alignment Scores:
Pred. No.:
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Sequence 17, Application US/10042894A

Publication No. US20030009011A1

GENERAL INROMATION:

APPLICANT: Shi, Jinrui

APPLICANT: Beach, Larry

APPLICANT: Reach, Larry

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

APPLICANT: Cahoon, Rebecca E.

TITLE OF INVENTION: No. US20030009011A1e1 Inositol Polyphosphate Kinase

TITLE OF INVENTION: Genes and Uses Thereof

TITLE OF INVENTION: US/10/042,894A

CURRENT APPLICATION NUMBER: US/10/042,894A

CURRENT FILING DATE: 2002-01-09

PRIOR FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                GlyValArgValValGlyProGlu---GlyAlaValTrpArgThrGluArgProGluVal 160
                                                                                                                                                                                                                                                                                                                                                                                        200
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                                                                                                                                                                                                                        102 ValAlaAspileLysIleGlyAlaIleThrTrpProProSerSerProGluProTyrIle 121
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                                                     42 GluHisGluValAlaPheTyrGluAlaPheSerAlaHisAlaAlaValProAlaArgIle 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 GlyGlyGlyValThrValLysLeuValAspPheAlaHisValAsgGlyVal
              181 AspGluGlyMetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyUyBGlyGlyValLeu
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Sovalic, David K.
APPLICANT: Sov, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Burbazuk, Brad
APPLICANT: Birbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
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                                                                     crgaagggarcgacgccgccgcgcgcgcgcgcgcccccccaacgccccacggc
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Matches:
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ORGANISM: Oryza sativa
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Publication No. US2030009011A1
GRNERAL INFORMATION
APPLICANT: Shi, Jinrui
APPLICANT: Bacch, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
TITLE OF INVENTION: No. US20033009911A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
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LOCATION: (1)...(643)
OTHER INFORMATION: n = A, T, C
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows
SEQ ID NO 17
LENGTH: 643
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ORGANISM: Zea mays
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US-10-042-894A-13
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PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Ve;
SEQ ID NO 13
LENGTH: 1020
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US-10-042-894A-13
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Pred. No.:
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APPLICANT: Shi, Jinrui
APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: No. US20030009011A1el Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 GlyValLeuSerGlnLeuArgGluLeuLysAlaTrpPheGluGluGlnThrLeuPheHis 217
                                                                                                                                                                                                                                                                       218 PheTyrSeralaSerIleLeuLeuGlyTyrAspAlaAlaAlaValAlaAlaGlyGlyAsp 237
                                                    143 Valargvalval --- GlyProGluGlyAlaValTrpArgThrGluArgProGluValLys
                                                                                 530 CTAAGGGTATATCAAAATAGCGAAGCTGGATTTTGGCAACCTGAGAAGAAGGTTGTTAT
                                                                                                                    162 AlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSerValAlaAsp
                                                                                                                                                                                                         238 GlyGlyGlyValThrValLysLeuValAspPheAlaHisValAlaGluGlyAspGlyVal
                                                                                                                                     182 Glugiy------MetAspCysAlaLeuAjaAlaAalaValTyrGlyGlyLysGly
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Conservative:
Mismatches:
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62.72%
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LOCATION: (12)...(851)
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Best Local Similarity:
Query Match:
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Sequence 11, Application VO. US20030009011A1

GENERAL INCORMATION:
APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Oc. US20030009011A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Oc. US20030009011A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
TITLE OF INVENTION: Genes and Uses Thereof
CURRENT FILING DATE: 2002-01-09
PRIOR PILING DATE: 2002-01-09
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11
LEMOTH: 1195
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CTCAAGGTCCCGGATCATCAAGTCGCCGGTCACCGGGGAGACGGGGAAAGCTGGGGCCA 178
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     GGTGCT----CGGTCAAACGCAGAAGTCAAACTTATTGATTTTGCTCATGTTACAGATGGT 791
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                                    255 AspGlyValIleApHisAsnPheLeuGlyGlyLeuCysSerLeuIleLysPheValSer
                                                                     792 AATGGTGTTATTGATCACAATTTCTTGGGTGGGCTCTGTTCTTTGATAAAGTTCATTTCT
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852 GACATACTTTCGGAGACA 869
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47.50%
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ORGANISM: Eucalyptus grandis
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US-10-042-894A-11
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                     27 GlySerGlyLeuPheTyrLysProLeuGlnAlaGly------AspArgGlyGlu 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            976 GATCACAACTTCTTGGGTGGCCTTTGTTCCTTCAAGTTCCTCAAGGATATCCTA 1032
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                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                          FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_67156C.1
US-10-424-599-106467
                                                                                             6.47e-67
644.50
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                                                                                                                                         Best Local Similarity:
 TYPE: DNA
ORGANISM: Glycine
                                                                                                                            Percent Similarity:
                                                                                    Alignment Scores:
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Expurithua
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 106467
LENGTH: 1345
                                                                                                                              257
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|||CTCAAG------GACTCTATCTCCTCGGAACCTACCAGGAATCTCTCCAGTGT 485
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ProGluHisGlnValAlaGlyHisArgAlaSerAlaSerLysLeuGlyProLeuIleAsp
                                                                                                             43 HisGluValAlaPheTyrGluAlaPheSerAlaHisAlaAlaValProAlaArglleArg
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US-10-425-115-74436
; Sequence 7436, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: ADAU, Yihua
; APPLICANT: CAO, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21 (5322) B
; CURRENT APLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 74436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 AlaGluGlyAapGlyVallleAapHisAanPheLeuGlyGlyLeuCysSerLeulleLys 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-042-894A-8 (1-289) x US-10-425-115-74436 (1-776)
                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                NAME/KEY: unsure;
LOCATION: (1)..(776)
COTHER INFORMATION: unsure at all n locations FEATURE;
OTHER INFORMATION: Clone ID: MRT4577_167884C.1
US-10-425-115-74436
                                                                                                                                                                                                                                                                                                                                                      5.73e-63
609.00
100.00%
99.15%
40.04%
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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Pred. No.:
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completed: June 17, 2005, 09:05:18 Search cor Job time

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Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 27, App Sequence 27, App Sequence 1131, A Sequence 1208, Ap Sequence 1208, Ap Sequence 1265, Ap Sequence 1265, Ap Sequence 1555, Ap Sequence 1559, Ap Sequence 1122, App Sequence 1122, App Sequence 1122, App Sequence 1122, App Sequence 1129, Ap Sequence 1129, Ap Sequence 1129, Ap Sequence 1509, Ap Sequence 1614, Ap Sequence 1621, Ap

Sequence 914, App Sequence 1091, Ap Sequence 1218, Ap Sequence 2, Appl

OM protein

Run on:

Sequence:

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FOR THE DETECTION OF BLOOD CELL GENE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
COMPUTER: PC-DOS/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRICATION NUMBER:
FILING DATE:
FLING DATE:
FLING DATE:
FLING DATE:
FLING BATE:
FLING BAT
                                                                                      PCT - US54 - 10166 - 6

3 US - 09 - 103 - 440A - 1

US - 08 - 131 - 731A - 132

US - 08 - 252 - 991A - 11331

US - 09 - 202 - 540 - 927

US - 09 - 902 - 540 - 4178

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US - 09 - 902 - 540 - 1059

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US - 09 - 949 - 0105 - 1359

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US-09-902-540-1218
US-09-103-840A-2
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US-09-023-655-809
; Sequence 809, Application US/09023655
; Patent. No. 6607879
; GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALL ALIFORNIA
COUNTRY: USA
ZIP: 94304
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1001
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  Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
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-QGA12_11/05FO_GPD01/VG1042804_TRN_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FERSE_FER
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712, 7
103, 7
102, 8
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5436,
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1521
1 MSDLHPPEHQVAGHRASASK.....IKFVSDIVPETPHTQPLGPS 289
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/ptTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/ptTUS_COMB.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                        June 17, 2005, 03:46:13 ; Search time 205
                                                                                                                          - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-023-655-809
US-09-620-312D-712
US-09-774-528-103
US-09-774-528-103
US-09-949-016-4634
US-09-248-796A-5436
US-09-248-796A-5436
US-09-949-016-2348
US-09-949-016-2348
US-09-248-796A-4664
US-09-248-796A-4664
US-09-252-991A-12872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Ygapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match
                                                                                                                                                                                                                                                                         Title:
Perfect score:
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189
182
178.5
145.5
113.5
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112.5
1008
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Database

Result

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821 TGGTCATTTATGATGGCAAGGAGCGGCCCGAAGTGGTCCTGGACTCAGATGCTGAGGATT 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 712
                                                                                                                                                                                                                                                                                                                Sequence 712, Application US/09620312D
Patent No. 6569662
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45.27%
29.22%
12.43%
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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US-09-620-312D-712
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o-HisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaProCysValAlaA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 ACCTCAAGATGGGCACACGACAACATGGTGATGATGCTTCAGAGGAGAAAAGCAGCAGCCAACC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 ysLeuAlaLysAspArgGlyThrThrSerValLeuLeuGlyPheArgValSerGlyValA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 rgValValGlyProGluGlyAlaValTrpArgThrGluArgProGluValLysAlaMetA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 AGGTGTAC-----CAAGCAGCAG-TGGGCAGCTCATGTTCATGAACA-AGTACCATGG 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spThrAlaGlyValArgArgValLeuArgArgTyrValSerSerValAlaAspGluGlyM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 etAspCysAlaLeuAlaAlaAlaValTyrGlyGlyLysGlyGlyValLeuSerGlnLeuA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||||::|
717 GTACCTGGGGCGTG------AACTCCTG-GGCCCTGTGCTCAAGAAGCTGA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 rgGluLeuLysAlaTrpPheGluGluGlnThrLeuPheHisPheTyrSerAlaSerIleL 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 T-------GAAGGAGAATGCAAAGCATCGGAACC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spilelysileglyAlaileThrTrpProProSerSerProGluProTyrileAlaLysC 124
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                                                                                                                                                                                                                                                                                                                                                            8 GluHisGlnValAlaGlyHisArgAlaSerAlaSerLy8-LeuGlyProLeuIleAspGl
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                           27 ySerGlyLeuPheTyrLysPro------
                                                                                                                                                                                                                        Length:
           TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 809:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT01
CLONE: 753522
 (650) 855-0555
                                                                                                                                                                                                                                193.00
40.36%
26.11%
12.69%
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Best Local Similarity:
Query Match:
DB:
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1001 ATGGCGAGGACACCGTGGTGCATGAGGGCCAG------GATGCTGGCTATATCTTCG 1051
                                        881 TGGAGGACCTGTCAGAGGAATCAGCTGATGAGTCTGCTGGTGCTCTATGCCTACAAACCCA 940
                                                                                                                                                               -----ValAlaGluGlyAspGlyValIleAspHisAsnPheLeuGlyG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 --AspGlyGlyGlyValThrValLysLeuValAspPheAlaHis------
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---AlaAlaAlaValAlaAlaGlyGly-
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APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwai
APPLICANT: Wang, Zhiwai
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
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Matches:
Conservative:
Mismatches:
Indels:
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NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_Ft_genes Version 2.0
SEQ ID NO 103
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                                                                       TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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; NAME/KEY: CDS
; LOCATION: (367).
US-09-774-528-103
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Pred. No.:
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                       eGlnAlaProCysValAlaAspIleLysIleGlyAlaIleThrTrpProProSerSerPr
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APPLICANT: Bundi, Vinod
APPLICANT: Bundi, Vinod
APPLICANT: Bundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Wenny, Yonghong
APPLICANT: Wengi, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: DINENTION: No. 6743619e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
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US-109-49-UL6-463-4

Sequence 4634, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOON 1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPIOR RELING DATE: 2000-10-03
SOUTHARE: FREESEQ for Windows Version 4.0
SEQ ID NO 4634
LENGTH: 1781
                LeuAspAspLeuLeuAlaGlyPheGlnAlaProCysValAlaAspIleLysIleGlyAla 109
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-4634
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TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: DL FL genes Version 2.0
SEQ ID NO 102
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                            Sequence 102, Application US/09774528
Patent No. 6743619
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                                                                        Tang, Y. Tom
Zhou, Psing
Goodrich, Psing
Isiu, Chenghua
Asundi, Vinod
Ren, Feiyan
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                           GENERAL INFORMATION:
APPLICANT: Tang, Y
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Pred. N. Score: Score: Percent Best Lo Query M. US-10-0.  Ob Db	6 8 6 8 6 8 6	3 4 5 4 5 4 5	3 6 8 6 8 6 8	8 8 8 8 8 8 8 8					
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| Sequence 2348, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANIT VEWTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT FILING DATE: 2000-00-41,755 |
| PRIOR PELICATION NUMBER: 60/241,755 |
| PRIOR PELICATION NUMBER: 60/241,756 |
| PRIOR PILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SCOFTWARE: FastSEQ for Windows Version 4.0 |
| LEMITH 44946
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    174 rgTyrValSerSerValAlaAspGluGlyMetAspCysAlaLeuAla-----AlaAlaV 192
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                                                                                         --AlaGlyValArgArgValLeuArgA
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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US-09-949-016-2348
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US-09-949-016-2348
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RESULT 7
US-09-252-991A-6525/c

US-09-252-991A-6525/c

Sequence 6225, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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Mismatches:
Indels:
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Matches:
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113.50
33.51%
24.35%
7.46%
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Best Local Similarity:
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 323
TYPE: DNA
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112.50
34.98%
20.85%
7.40%
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Query Match:
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US-09-949-016-323
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER,
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REPERENCE: CLO1307
CURRENT PAPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                     1026 GAGGAAAAAGCACAGCGGGTGTGACCAAGCCACGGTACATGCAGTGGCGGGAGACCATC 1085
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906 TGCAAGATGGGAATCAGGACCTACCTGGAGGAGGAGCTCACGAAGGCCCGGAAGAAGAAGCCC 965
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                                                                                                       PhePheProArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnProGlyGluPro
                                                                                    HisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaProCysValAlaAsp
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: NUCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
NUMBER: OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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                 114 oSerSerProGluProTyrIleAlaLysCysLeuAlaLysAspArgGlyThrThrSerVa 134
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                                            2449 grccccccaecaccaecregregedgacecccccccccaagaagac--
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Best Local Similarity:
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                               271 LysPheValSerAspIleValProGluThrPro
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LOCATION: (1)..(14555)
OTHER INFORMATION: unsure at all
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Qy         57 ValProalaArgileArgAspThr	RESULT 12 US-09-252-991A-12872/C US-09-252-991A-12872/C  Sequence 12872, Application US/09252991A  Sequence 12872, Application US/09252991A  REPLICATION: More Settled et al.  APPLICATION: Marc J. Rubenfield et al.  APPLICATION: WICKLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  TITLE OF INVENTION: ABCUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  CURRENT APPLICATION NUMBER: US 60/074,788  PRIOR FILING DATE: 1998-02-18  PRIOR FILING DATE: 1998-02-18  PRIOR FILING DATE: 1998-07-27  NUMBER OF SEQ ID NOS: 33142  SEQ ID NO 12872  LENGTH: 984  LENGTH: 984  CORGANISM: Psecudomonas aeruginosa  US-09-252-991A-12872	Alignment Scores:  Pred. No.:  Pred. No.:  107.50  Matches:  Percent Similarity:  Best Local Similarity:  10.35  Best Local Similarity:  10.35  Best Local Similarity:  10.35  Best Local Similarity:  10.35  Best Local Similarity:  10.36  Best Local Similarity:  10.36  Best Local Similarity:  10.37  Indels:  Indels:

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2582 AGTCCTCACGCCAAACTGCAGGCGGTAGCCCAGCACCTGGTCCTCGGGGTGCCAGCCG 2523
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APPLICANT: RODAN, GIDEON A.
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2473 -CAGGGTTGGGCGGCCCAGCACTGCTCCTTGGTCACAACCAC
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APPLICATION NUMBER: US/08/348,006B
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126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
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Patent No. 5658756
                                                           161 sAlaMetAspThrAlaGlyVal
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STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 77,071
TELECOMMUNICATION INFORMATION:
TELECHOME: (650) 855-055
INFORMATION FOR SEQ ID NO: 1132:
SEQUENCE CHARACTERISTICS:
LENGTH: 4078 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.106
107.50
33.53%
24.25%
7.07%
                                                                                                             HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                             FILING DATE: HEREWITH CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER:
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US-09-016-434-1132
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Best Local Similarity:
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                                         35 LeuGlnAlaglyAspArgGlyGluHisGluValAlaPheTyrGluAlaPheSerAlaHis
                    240 -GlyvalThrvalLysLeuValAspPheAlaHisValAlaGluGlyAsp---GlyValIl
                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08800825A
; Patent No. 5865397
; GENERAL INFORMATION:
; APPLICANT: ROTHEDON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: SCHMIDT, AZRIEL
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: LIAC E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3077 AGTICITGGGCGAGACTIGGICCCGCAGGAACGTCCGGTAGCGGA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
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Matches:
Conservative:
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Indels:
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FILING DATE: 14-FEB-10.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: 14NN, 0. MARK
REGIGTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1899;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 723-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6000 base pairs
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STRANDEDNESS: single
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ZIP: 07065-0900
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STATE: NEW JI
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TGGGTTTGCTGCGGGGCGCATCGCCCTTCATGGTGTAGGCGGCTACCGTGATGGAGTACG 2370
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Matches:
Conservative:
Mismatches:
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SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: CDNA
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106.50
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24.24%
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Best Local Similarity:
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y 55AlaAlaValProAla-ArgIleArgAspThrPhePheProArgPheHi 70    ::	y         70 sGlyThrArgLeuLeuProThrGluAlaGlnPro	y 82GlyGluProHisProHisLeuValLeuAspAspLeuLeuAlaGl 96	y 96 yPheGlnAlaProCysValAlaAspIleLysIleGlyAlaIleThrTrpProProSerSe 116	y 116 rProGluProTyrIleAlaLysCysLeuAlaLysAspArgGlyThrThrSerValLeuLe 136 	y 136 uGlyPheArgValSerGlyValArgValVal146       ::   2762 GAATCTGCGGGTGGCCACGGGGGTTCCTCCGGATGCTCAGGACCTCGGCTCCT 2703	y 147GlyProGluGlyAlaValTrpArgThrGluArgProGluValLy 161	y 161 sAlaMetAspThrAlaGlyVal	y 170 gvalLeuargargTyrValSerSerValAlaAspGluGlyMetAspCy 186	y 186 sAlaLeuAlaAlaAalaValTyrGlyGlyLyVsGlyGlyValleuSerGlnLeuArgGluLe 206	y 206 uLysAlaTrpPheGluGluGluGlnThrLeuPheHisPheTyrSerAlaSerIleLeuLe 225 ::	y 225 uGlyTyrAspAlaAlaValAlaAlaGlyGlyAspGlyGlyAspGlyGly	y 240 -GlyValThrValLysLeuValAspPheAlaHisValAlaGluGlyAspGlyValI1 258	y 258 eAspHisAsnPheLeuGlyGlyLeuCysSerLeuIleLysPheValSerAspIleValPr 278	y 278 oGluThrProHisThrGlnProLeuGly 287	b 2249 CGCGGATCTGGCCGTGCTGCCGGG 2222
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Search completed: June 17, 2005, 06:38:38 Job time: 230 secs

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Aad43519 P. argent
Aac43516 Eucalyptu
Aac49750 Arabidops
Aac31685 Arabidops
Aac39023 Arabidops
Aac39023 Arabidops
Aac38692 Arabidops
Aac38692 Arabidops
Aad43520 Maize ino
Aad43520 Maize ino
Ad43521 Maize ino
Ad435306 Drosophil
Ab123306 Drosophil
Ab123307 Drosophil
Ab123307 Drosophil
Ad56742 Human ino
Ad66742 Human cDN
Ad66742 Human cDN
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Ad69042 DNA encod
Ad687184 Human pol
Ad699042 DNA encod
Ad6891 Human pol
Ad689042 DNA encod
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Ad64808 Human eec
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Ad66748 Human ORF
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Abx70876 Novel hum
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Abx883730 Human ino
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/product= "Maize IPPK protein #4"
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AAD43514
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-Q0=/Cgn2_1/USFTO_epool/US10042894/runat_15062005_111949_8281/app_query.fasta_1.455
-Q=/Cgn2_1/USFTO_epool/US10042894/runat_15062005_111949_8281/app_query.fasta_1.455
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-DB=N Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 - END=-1 -MARTIX=blosum62 - TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIND=0 -ALIGN=10
-USER=-US1042894 @CGN 1 1 470 @runat_15062005_111949_8281 -NCFU=6 -ICFU=3
-NO MANP -LARGEQÜERY -NRGC SCORES=0 -WAIT -NSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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1 MSDLHPPEHQVAGHRASASK.....IKFVSDIVPETPHTQPLGPS 289
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                  - nucleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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Jatabase

Minimum DB E Maximum DB E

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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polymucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The present sequence is maize IPPK DNA
                                                                                                                                                                            ValThrValLysLeuValAspPheAlaHisValAlaGluGlyAspGlyValIleAspHis 260
GACGAGGGGATGGACTGTGCGCTCGCCGCGGTGTACGGAGGAAAAGGTGGAGTCTTG 651
                                                        TCACAGCTGCGCGAGCTCAAGGCGTGCTTCTAGAGGAGCAGACTCTGTTCCACTTCTACTCG
                                                                                                                             GTGACGGTGAAGCTGGTGGACTTTGCCCATGTGGCCGAGGGTGATGGGGTGATTGACCAC
                                                                                                                                                                                                                                                                           SerGlnLeuArgGluLeuLysAlaTrpPheGluGluGlnThrLeuPheHisPheTyrSer
                                                                                                        AlaSerIleLeuLeuGlyTyrAspAlaAlaAlaValAlaAlaGlyGlyGlyGlyGlyGlyGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phytic acid;
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nutritional value, animal feed, transgenic, gene, ds
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                                                                                                      New inositol polyphosphate kinase polynucleotides and polypeptides, useful in medulating phytic acid biosynthesis by decreasing phytate increasing non-phytate phosphorous to improve the nutritional value animal feed.
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                  Rafalski
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate thair activity and raising anti-idiotypic antibodies. The present sequence is maize IPPK DNA
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                                                                                                                Maize; enzyme; inositol polyphosphate kinase; IPPK; |
nutritional value; animal feed; transgenic; gene; ds
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                     AAD43512 standard; DNA; 923
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in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polymucleotides of the invention are to produce transgenic plants with altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The present sequence is maize IPPK DNA
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Mismatches:
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nutritional value; animal feed; transgenic; ds.
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New inositol polyphosphate kinase polynucleotides and polypeptides, useful in modulating phytic acid biosynthesis by decreasing phytate increasing non-phytate phosphorous to improve the nutritional value
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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P-PSDB; AAE26200.
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Best Local Similarity:
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nutritional val
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Query Match:
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595 GAANGCTATGGACACCCGTCGGNGNCCGGCGNGTGCTTCGG
                        160 lLysAlaMetAspThr-AlaGlyValArgArgValLeuArg
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P-PSDB; AAE26199.
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The present sequence is P. argentatum IPPK DNA
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nutritional value, animal feed, gene, ds.
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                                                             143 ValArgValVal --- GlyProGluGlyAlaValTrpArgThrGluArgProGluValLys 161
                                                                                                                                        162 AlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSerValAlaAsp 181
                                                                                                                                                                                                                            182 GluGly-------MetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyLysGly 197
                                                                                                                                                                                                                                                                                                             GlyValLeuSerGinLeuArgGluLeuLysAlaTrpPheGluGluGlnThrLeuPheHis 217
                                                                                                                                                                                                                                                                                                                                                                                              PheTyrSerAlaSerIleLeuLeuGlyTyrAspAlaAlaAlaValAlaAlaGlyGlyAsp 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 GlyGlyGlyValThrValLygLeuValAspPheAlaHisValAlaGluGlyAspGlyVal 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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05-MAR-1999;
09-MAR-1999;
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25-MAR-1999;
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28-APR-1999;
30-APR-1999;
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	Length: 1130 Matches: 150 Conservative: 39 Mismatches: 82 Indels: 8 Gaps: 8	GlnValAlaGlyHisArgAlaSerAlaSerLysLeuGlyPro 23 	LeulleAspGlySerGlyLeuPheTyrLysProLeuGlnAlaGlyAspArgGlyGluHis 43    :::     CrGTAGATGACCAAGGCCGGTTCTTCAGGCAGAGAGATTCTCGTGGCGAACAC 213	eTyrCluAlaPheSerAlaHisAlaAlaValProAlaArgIleArgAsp 63           	eProArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnProGlyGlu 83      :::         ::    :::  CCCGGTGTATCACGCCACTCAGCTAGTTGAAGCATCTGATGATCT 324	alLeuAspAspLeuLeuAlaGlyPheGlnAlaProCysVal 102	AlaaspileLysileGlyAlaileThrTrpProProSerSerFroGluProTyrileAla 122    :::       :::	LyscysLeuAlalysAspargGlyThrThrSerValLeuLeuGlyPheArgValSerGly 142        :::	ProGluGlyAlaValTrpArgThrGluArgProGluValLys 161	1yalargargvalLeuargargTyrvalSerServal 179 		
99US-0160767P 99US-0160768P 99US-0160710P 99US-0160815P 99US-0160981P 99US-0160981P 99US-0161468P 99US-0161468P 99US-016136P 99US-016136P 99US-016136P 99US-016136P 99US-016136P 99US-016136P 99US-016136P 99US-016136P 99US-016136P	2.29e-56 714.50 i. 66.55\$ ity: 52.82\$ 46.98\$ 3	sProProGluHis          3GTCCTGAACAC	1easpGlySerGly   -::      stagargaccaaggc	GluvalAlaPheTyrGlu      AGGCTAAGTTCTATGAG	접그타	ProHisProHisLeuValL           GGCAAGCTTCCTCATCTTGTTC	AspileLysileGly     :::         SATGTTAAGATTGGA	CysLeuAlaLysAspi     :::  GTATTAAGAAAGATi	ValArgValValGly   :::  TTAAGATTTTGATCAC	AlaMetAspThrAlaGlyVal ::: GGGTATAATGCAGATGGTGCT	aAspGluGlyMet      ::: :TGACTCTAACTTGACA	.yvalLeuSerGlnLeu  :::      ;garcrragcGcAGrrG
21-0CT-1999; 21-0CT-1999; 21-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999; 25-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 28-0CT-1999; 28-0CT-1999; 28-0CT-1999;	Scores:   milarit   Similarit   Similarit   Similarit	4 LeuHie     94 CTCAAC	24 Leul    :   54 CTCC	44 Gluv     214 GAGC	64 ThrPhe ::: 271 AGATAC	84 ProHi	103 AlaA 385 ATGC	123 LyBC        445 AAA	143 Val <sup>2</sup> 505 TTT	162 AlaN 565 GGG7	180 AlaA      625 GCTC	198 GlyVa    : 685 GGGAT
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    Hybridisation assay, genetic mapping, gene expression control; protein identification; signal transduction pathway; metabolic pathway;
    PheTyrSeralaSerIleLeuLeuGlyTyrAspAlaAlaAlaVal---AlaAlaGlyGly
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242 CTCGTAGATGACAAGGGTCGGTTCTTCAAGCCACTTCAGGGCGATTCTCGGGGTGAAATC 301
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Or polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The
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                                                                                                                                                                                    Soybean, enzyme; inositol polyphosphate kinase; IPPK; phytic acid; nutritional value; animal feed; transgenic; gene; ds.
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                                                                                                                                      Soybean inositol polyphosphate kinase (IPPK) DNA
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standard;
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        ---CCCCACCCTCACCTGGTCCTGGAGACCTCTGCGGGCTACTCCAAACCCTCCGTC 314
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Search completed: June 17, 2005, 04:11:12 Job time : 625 secs

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BT011900 AC124954 AY147935 ATH404678

AC127018 AP004981

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clade, Panicoideae, Andropogoneae, Zea.
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AUTHORS
TITLE
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AX513568 Sequence
AX513566 Sequence
AX513564 Sequence
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                        nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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YSASILLGYDAAAVAAGGDGGGVTVKLVDFAHVAEGDGVIDHNFLGGLCSLIKFVSDI
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Sequence 5 from Patent W002059324.
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Shi,J., Beach,L.R., Wang,H., Rafalski,J.A. and Cahoon,R.E.
Novel: inositol polyphosphate kinase genes and uses thereof
Patent: WO 02059324-A 20 01-AUG-2002;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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/product="hypothetical protein"
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TTVTVKWRGKPVFIRRTEEDINLANSVDIGSLRDPQQDAERVKNPEWLVVIGVCTHL
GCIPLPNAGDFGGWFCPCHGSHYDISGRIRKGPAPYNLEVPTYSFLEENKLLIG"
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/gene="OSJNBa0047A17.6"
/complement (join(18932. .19648,19740. .19836,20081. .20194,
20280. .20444,20690. .20827,20923. .20999,21093. .21207,
21277. .21382,21703. .21764,21859 .21993,22149. .22331,
22880. .22936,23369. .23417,23504. .23652,24724. .24771,
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probably inactive due to including stop codon(s) in CDS"
join(15870. 16043,16479. 16484)
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/mol_type="genomic DNA"
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/db_xref="taxon:39947"
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/note="Rieske iron-sulfur protein
/note="Rieske iron-sulfur protein
/contains EST(8): AU162572 (C63256), AU068962 (C51210)
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complement(11599. .12180)
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/note="Bupported by full-length cDNA(s): AK120851"
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predicted by GENSCAN
this category is not included in IRGSP standard"
complement(5864, .9107)
/gene="OSJNBa0047A17.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               included in IRGSP standard"
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Gene="CSNDBa0047A17.3"
join(+9904. .10067,10732. .>10750)
gene="OSJNBa0047A17.3"
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                                                                                                                                                                            /gene="OSJNBa0047A17.1"
join(2637...2780,3298...3360)
/gene="OSJNB0,3298...3360)
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complement(<11599. .>12180)
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join(2637. .2780,3298.
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complement (18932. .25
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Direct Submission

Direct Submission

Submitted (18-SEP-2002) Takuji Sasaki, National Institute of Agrobiogical Sciences, Ricc Genome Research Program, Kannondai 21-12. Taukuba, Ibazaki 305-8602, Japan Research Program, Kannondai (E-mail:taasakienias affrc.go.jp, URL:http://rgp.daa.affrc.go.jp, URL:http://rgp.daa.affrc.go.jp, URL:http://rgp.daa.affrc.go.jp, URL:http://rgp.daa.affrc.go.jp, URL:http://rgp.daa.affrc.go.jp, URL:http://rgp.daa.affrc.go.jp, URL:http://rgp.daa.affrc.go.jp, URL:htm], FERNESH (http://rgp.daa.affrc.go.jp/st.cehWh/), SpicePredictor (http://www.iigr.org/software/glimmerm/), BlackTW and BlackTW (http://globin.cse.psu.edw)htm]/dccs/simd.htm]), gabc.database at Reg or Doby. Protein homologies of the cohresponding Doby accession no. and Rop clone ID. Full-length cohras represent the identified cDNA sequences using BlackTW with the corresponding Doby accession no. and Rop clone ID. Full-length cohras represent the identified cDNA sequences using BlackTW with the corresponding Doby accession no. and Rop clone iD. Rassified as an 'unknown' protein 'A gene without assame name, 'Putative-' and -like protein' A gene without significant homology to ap protein but with identify of partial sequence is fature of the sequence is from -like protein a probable 'hypothetical' protein according to IRGSP standard, A gene with deather a same na
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Peprantophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                  260 sAsnPheLeuGlyGlyLeuCysSerLeuIleLysPheValSerAspIleValProGluTh 280
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OSJNBa0047A17
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Direct Submission
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                                                                                                                                                147200 TCCGACCTGCCCCCCCCGGAGCACCAGGTGGCGGGGGCACCGCGCGTCCGCCGACAAGCTG
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                                                                                                                  SerAspleuHisProProGluHisGlnValAlaGlyHisArgAlaSerAlaSerLysLeu
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GKHDLIGKIVKSVAELEKMYHSQDGENFVPASTAHDSHSKEVLKSQVYVEKYLENNR
QTFLDYSTSAGGCGLNFWANDVDFTASNGNREPPSLHYTIDTGRRPNYQRALLEWGUNLQ
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VYGYGGADFKERREFLDPNKGERLESSTGRVASRDMIQFAPMKDAHGSGISTVQSLLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(26913. .27610,27708. .29002,29099. .29157,29238. .29264)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement (26424. .26747)
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218
21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="predicted by GENSCAN etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I PGQFMTYMRTREIQAIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon start=1
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1148.50
84.45%
77.03%
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Pred. No.:
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           CDS
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Oryza sativa (japonica cultivar-group)

GI:49388255

AP004772.3

ACCESSION VERSION KEYWORDS SOURCE

Percent Similarity: Best Local Similarity:

Query Match:

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/ LTAINS ALONG WALD DENDE AND A SAFITKLOLS VSDGLPHAAP VPELSTOE
HELVKS VFEVLOGFDTVLLYNDKTA PGYCEKAGIT VVSHLSQTSLRAVLK PFLFRAATCL
KOYDE LVGKRYRS CGHOTPTLAS PRASY VSDWLMKIRK KAALKEE EGOLF LEVSVERTITLIGE
TDSMSSLCSGAREHLYOVOGAN PODE WINSGAQMASS BY VARHANHEKKLING VERSTELLEGE PHINLL VIFAGTILL PYLOCLDSMLYDGILLD PINEEM FYANKAVTID QAFWEN
SYMLKYNG PRETDSSSTLADNES IRKKELINO STTAAAALLKS SNOGGADILC PVFLKD
IARAILSAGKS PQLVQUVQ STHRIQTREVIHEFNID OHGNYIS QQKFR PDTSSIT NOB
KREDIIESSTGOP GANNACK MOPTILLSSF LICLSGLLENG PHYDDYLRKLCADINA PWI
KTIVHSKSNVQETESVCGENSSEKTWLKLLR PATSGLEGDEN AND REPETEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGDHQDVSSTEVESYFNLSCYENPGITACQEMLERNKNSWSDLNISKSPHLPPLNDEN
TRKSTFGDRDSSTTIGDTLSTTYFPRLDGTDYKFGPRDDSSETIROBSSTIROBDRRTLEALY
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KRQVDHIGKQILSKLMGDWRLMDELFVLRAIYLLGSGDMLQQFLVTIFDKLDKGNPWD
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ALDVLNFTYKVSWPLDIIVYTEALKKYYNQWAFLLKYKRAKFILDETRKWMKGGGST
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Tvsqegvgegvlegrgscqiivpch"
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19837. 20034,20118. 20288,20405. 20512,20611. 20829,
20914. 21120,21227. 21445,21564. 21638,21998. 22150))
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AU055859(S20105),AU085756(C52347),C27605(C52347),AU078722
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12870. .12980. 13240,13613. .13240,13513. .14053,
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                                                                             note="start and end point are not identified" oin(6065. .6067,6850. .7404)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon start=1
              mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-12, Tsukuba, Ibaraki 305-8662, Japan

1-12, Tsukuba, Ibaraki 305-8662, Japan

E-mail:tessaki@nias.affcr.go.jp, URL:http://rgp.dna.affcr.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jun 28, 2004 this sequence version replaced gi:37497094.

Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were futp://www.tigo.org/fcd/gi/mmerm/gi/merm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mmerm/gi/mme
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probably inactive due to including stop codon(s) in CDS probably inactive due to too long 3'UTR in CDS"
                                                                                                                                                                                                                                                                                                                                                     Saski,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (20-FEB-2002) Takuji Sasaki, National Institute of
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/doltivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="2"
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/gene="P0415B12.1"
/note="supported by full-length cDNA(8): AK121467"
/gene="P0415B12.1"
                                                                                                                                                                                                                            chromosome 2, PAC
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                                                                                                                                                                                    Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                           Published Only in Database (2002)
2 (bases 1 to 157419)
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complement":
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/gene="P0415B12.2"
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                                                                                                                                                                                                                                                         clone: P0415B12
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The Rice Pull-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, M., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunda, Y., Kurossaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Kusumegi, T., Oka, M., Rwamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Alzawa, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Macuni, K., Ishii, Y., Itoh, M., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
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FLI CDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Bhrhartoideae, Oryzeae, Oryza.
---GlyGluProHisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaPro 100
                                                                                                                                                                                                                      SerGlyValArgValValGlyProGlu---GlyAlaValTrpArgThrGluArgProGlu
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/gene="P0415B12.5"
join(25322. .25357,28498. .28641)
/gene="P0415B12.5"
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/product="hypothetical protein"
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2 (Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pudachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Haranto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, T., Hotta, I., Iida, Y., Iida, Y., Ishia, W., Imamura, K., Haranto, T., Iida, Y., Ishikawa, M., Imamura, K., Hotta, I., Iida, Y., Ishikawa, M., Imamura, K., Kabikawa-Hirozane, T., Kawamata, M., Kawamata, M., Kawamata, M., Kawamata, M., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kobayashi, M., Koya, S., Kurihara, C., Kurosaki, T., Miura, J., Miyazaki, A., Masuba, H., Matsuyama, T., Miura, M., Miyazaki, M., Mamiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohned, W., Ohneda, E., Ohno, M., Ohtsuki, K., Sasto, K., Sato, K., Sato, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Suzuki, K., Solabe, Y., Sugamo, R., Suzuki, K., Suzuki, Y., Tagami, T., Tamara, T., Tomaru, A., Tayama, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Falls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fuls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fuls Genome Sequencing & Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kuroaski,T., Kusumeaj,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Milkura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Masubara,K. and Murakami,K. Genome Exploration Research Group in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carnind,P., Fukuda,S., Hanamoto,K., Hara,A., Hashizume,W., Hayashida,K., Haratu,M., Hashizume,W., Hayashida,K., Haratu,M., Kanagawa,T., Kondo,S., Konno,H., Kouda,M., Kayawa,T., Kanagawa,S., Kacho,H., Kawai,J., Koha,M., Sakawa,T., Miyazaki,A., Murata,M., Nahi,K., Nomura,K., Numasaki,A., Ohno,M., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sakai,C., Sakai,K., Sakazume,N., Tagami,M., Tagami,M., Tagami,T., Towaru,A., Toya,T., Waki,K., Tagawa,A., Takaka-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Toya,T., Waki,K., Yasunishi,A., Tagami,Y., Tomaru,A., Toya,T., Waki,K., Toya,T., Waya,T., Waki,K., Yasunishi,A., Tagami,Y., Tomaru,A., Toya,T., Toya,T., Waki,K., Yasunishi,A.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagate,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
                                                                                                  Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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/moi type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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/clone="J023018G11"
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       Parthenium argentatum
Parthenium argentatum
Parthenium argentatum
Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheol
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids, campanulids, Asterales, Asteraceae, Asteroideae,
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/note="unnamed protein product"
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                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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DNA linear PLN 24-JAN-2002
Ngc-D, Ngc-A and Ngc-B genes.
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NGC-A gene; NGC-A protein; NGC-B gene; NGC-B protein; NGC-D gene; NGC-D gene; NGC-D gene; NGC-D gene; NGC-D gene; NGC-D gene; Nigo-D protein.

Linum usitatissimum

Linum usitatissimum

Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; resids; eurosids I; Malpighiales; Linaceae; Linum.
  LysCysLeuAlaLysAspArgGlyThrThrSerValLeuLeuGlyPheArgValSerGly 142
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                                                                      LeulleAspGlySerGlyLeuPheTyrLysProLeuGlnAlaGlyAspArgGlyGluHis
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TGSRTWYPEASEEYIQKCLEKDRNSTSVSLGFRISGLRVYQNSEAGFWQPEKKVVYSF
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/db_xref="GI:23559675"
/translation="MLKVPDHQVAGHRGDGGKLGPLVDDSGRFYKPLQSDHRGDTEVA
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Wararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, Myrtales, Myrtaceae, Eucalyptus.
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LeuPheHisPheTyrSerAlaSerIleLeuLeuGlyTyrAspAlaAlaAlaValAlaAla
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/note="unnamed protein product"
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/mol type="unassigned DNA"
/db_xref="taxon:71139"
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SKLSSLEFLALALTDSYKSDFTEMLPTSLTLLYISNDTQKFCPDTSSENLQRLPNLSN
LINLSVLYLIDVGIGEILGLGELKMLEYLSIGRASRIVHLDGLENLVLLQHLRVEGCR
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ELIEVPGLDALESLKWLSMEGCRSTRKVPDLSGLKKLKTLDVESCIQLKEVRGLERLE
SLEELKMSGCESIEELPNLSGLKNLRELLLKGCIQLKEVNGLEGLELTVFEARKRIKA
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                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-MAR-2001) Dodds P.N., Plant Industry, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia Location/Qualifiers
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/standard_name="n-X50"
/note="Site of 11 bp insertion in n-X50 rust susceptible
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/note="Sice of LUTE transposon insertion in n-X128A rust
susceptible mutant allele"
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/note="233 bp deletion in n-X139 rust susceptible mutant
Dodds, P.N., Lawrence, G.J. and Bllis, J.G.
Contrasting modes of evolution acting on the complex N locus for
rust resistance in flax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(2881. .3431,3533. .4652,4770. .5045,5140. .6519)
/gene="Ngc-D"
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/gene="Ngc-D"
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/protein id="CAC35321.1"
/db_xref="G1:1350920"
/db_xref="G08.0920"
/db_xref="CAS.09ARC4"
/db_xref="UniProt/TrEMBL:09ARC4"
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/product="hypothetical protein"
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/mol_type="genomic DNA"
/variety="Bombay"
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                                                                                      rust resistance in flax
Plant J. 27 (5), 439-453 (2001)
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/function="unknown"
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Dodds, P.N.
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join(20265. .20815,21104. .22202,22415. .22690,22818. .24218)
/gene="Ngc-B"
join(20265. .20815,21104. .22202,22415. .22690,22818. .24218)
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                                                                                                                                                                                                                                                                                                                                            .16493)
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| db_xref="UniProt/Tremal.goarc3"
| db_xref="UniProt/Tremal.goarc3"
| db_xref="UniProt | draw | 
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IGRWYVPBASQAYIBKCLKKOVESSPPLLGFRISGLQVYGNGKESSFVLLKPBKLL
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LQELAKWYDVWKNGGGGGKGQHIILPVFYFWDPRDVRHPDSGPYKEAFEGHNLKHDPET
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LELSGYGITNILPPSLSIYTKLKSLKVSDSQLPDLNLKNLRCLKIGGCDNFIEITGL
HTLESLEELRVMGSSIRKLDLTGLVKLEILQPDSCTQLTEIRGLGGLESLQRLHMSRC
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                                                                                                                                                                                                                                                                                                                                            join(12668. 13218,13450. 14542,14757. 15032,1518

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join(12668. 13218,13450. 14542,14757. 15032,1518

/gene="NgC-A"

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/db_xref="GOA:Q9ARC2"
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| protein | id="CaC35325.1"
| db_xref="G1:1350921"
| db_xref="GOA:Q9AR40"
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10276 TGTTCTGTTCTTATGCTGTATGAGAAGAGAGAAGACGAAGATGGTGAATGGAGGAGAAGA 10335
                                                                                                                                                           10396 GTTATCGATCACAACTTTCTTGGAGGGCTCTGCTCATTGATAAAGTTCATTTCGAGATC 10455
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Arabidopsis thaliana gene for inositol-(1,4,5) trisphosphate
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
----AspAlaAlaAlaValAlaAlaGlyGlyAspGly 238
                                                                                                                                                                                                                                                    257 ValileAspHisAsnPheLeuGlyGlyLeuCysSerLeuIleLysPheValSerAspIle
                                                                                                                       -----GlyGlyValThrValLySLeuValAspPheAlaHisValAlaGluGlyAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xia, H.J., Brearley, C. and Mueller-Roeber, B.
Identification of inositol-(1,4,5) trisphosphate 3-kinase from Arabidopsis thaliana
Unpublished
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Direct Submission
Submitted (09-JUL-1999) Xia H.J., AG Mueller-Roeber,
Max-Planck-Institute of Molecular Plant Physiology,
Karl-Liebknecht-Strasse 25, Haus 20, 14476 Golm, GERB
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Conservative:
Mismatches:
Indels:
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1. .903
7. Organism="Arabidopsis thaliana" /mol type="Genomic DNA" /marlety="Col"

    . 903
    function="phosphorylation of t'insitol-(1,4,5) trisphosphate"
/codon start=1

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                  277 ValProGluThrProHisThrGlnPro 285
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1. :903
   221 AlaSerIleLeuLeuGlyTyr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-kinase.
AJ243592
AJ243592.1 GI:14588984
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714.50
66.55$
52.82$
46.98$
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Query Match:
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Pred. No.:
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9685 GATTCAGGGCGATTCTACAAGCCACTTCAGGGCGATGAACGTGGGGGAACCGAGATGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 AlaLysAspArgGlyThrThrSerValLeuGlyPheArgValSerGlyValArgVal 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 AlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSer---ValAla 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 ProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaProCysValAlaAspIle 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 LysileGlyAlaIleThrTrpProProSerSerProGluProTyrileAlaLysCysLeu 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 ValGlyProGlu------GlyAlaValTrpArgThrGluArgProGluValLys 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ProArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnProGlyGluPro---His
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Matches:
Conservative:
Mismatches:
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66.78%
51.56%
47.24%
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Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Chenk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yang, C.C., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A.
Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Onodera, C.S., Ewal, Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (08-7AN-2002) Salk Institute Genomic Analysis Laboratory
SignAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA): 'RIKEN trabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldemith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palam, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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Pred. No. 6.8e-201;
; Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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/protein_id="CAD52954.1"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Sequence 1 from Patent W002059324.
AX513564 AX513564.1 GI:23559664
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Shi,J., Beach,L.R., Wang,H., Rafalski,J.A. and Cahoon,R.E.
Novel inositol polyphosphare kinase genes and uses thereof
Patent: WO 02059324-A 20 01-AUG-2002;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Pred. No. 1.5e-121;
0; Mismatches 21;
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Sequence 3 from Patent WO02059324.
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AX513566.1 GI:23559666
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 & 8	182 AGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCCGCCCGC	/mol_type="unassigned DNA" /db_xref="taxon:4577" 89424 /note:"innamed profesin produ
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ر که و	302 CGCATCCTCACCTCGACGACGACGACGCGGGGTTTCAGGCGCCCTGCGTGCG	VAFYERFSHAUPARIRDTFFENG VAFYERFSHAUPARIRDTFFENG ADIKIGAIT"
è 8	362 ACATCAAGATGGGGGCATCAGGGGCCACCGAGTTCGCCGGAGCCCTACATGGCCAAGT 421 	Query Match Best Local Similarity 88.7%; Pred. No. 7.5e Matches 802; Conservative 0; Mismatches
ò a	422 GCCTCGCCAAGGACCGCGGAGCGTTCTGCTCGGATTCCGCGTCTCCGGCGTCC 481	Oy 2 CACGAGGTCAGTCACCGTCACCCTCGCGCCCATAGT
ò a	482 GAGTCGTCGGCCCCGGAGGCGCCGTGTGGCGGAGCGCCCGGAGGTGAAGGCCATGG 541	Oy 62 TCCACCGGGGGGCACCAAGTCGCGGGCACCGGCACCGGCGGCACCGGCGGGGCACCGGCGG
÷ €	542 ACACCGCCGGCGTCGCCGCGTGCTCCGCCCTACGTGTCATCCG-TTGCCGACGAGGG 600	Oy 122 TCATCGACGGCTCCGGCCTCTTCTACAAGCGGCTC
è 8	601 ATGGACTGTGGCGCGGGGGGGGGGGGGAAAGGTGGAGGTTGTCACAGGTG 660 	Qy 182 AGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCC
<u>ک</u> ۾	661 CGCGAGCTCAAGGCGTGGTTCGAGGAGCAGACTCTGTTCCACTTCTACTCGGCGTCGATT 720 	Oy 242 CCTTCTCCCCGGTTCCACGGCACGCGACTCCT(
& a	721 CTTCTGGGCTATGATGCTGCTGCAGTCGCAGGCGAGATGGGGTGGGGTGACGGTG 780 	Oy 302 CGCATCCTCACCTCGACCACGACCTCCTCGCC
상 음 당	781 AAGCTGGTGGACTTTGCCCATGTGGCCGAGGGTGATGGGCTGATTGACCACAACTTCCTG 840 	Qy 362 ACATCAAGAICGGCGCATCACGTGGCCACCGAGT
S S	841 GGCGGGCTCTGCTCGTGATCAAGTTCTGACATTGTTCCGGAGACTCCTCATACG 900 	Qy 422 GCCTCGCCAAGGACCGCGGGACCACGAGCGTTCTC
cy qq	901 CAGCCTTTGGGTCCTTCTTAAGAGGATCCTGGGA-TTTCGATTTGATAACAAG 955 	Qy 482 GAGTCGTCGGCCCCGAGGCCCCGTGTGGCGGACC
RESULT 6 AX513578		Oy 542 ACACCGCGGCGTCCGCCGCGTGCTCCGGGGCTAAC
LOCUS DEFINITION ACCESSION VERSION	AX513578 899 bp DNA linear PAT 05-OCT-2002 Sequence 15 from Patent W002059324. AX513578 AX513578.1 GI:23559679	Oy 601 ATGGACTGTGCGCTCGCCGCGGGGGTGTACGGAGG 
KEYWOKDS SOURCE ORGANISM	.ea mays Zea mays Eukaryota; Viridiplantae;	Oy 661 CGCGAGCTCAAGGCGTGGTTCGAGGAGCAGACTCT
REPERENCE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1	Qy 721 CTTCTGGGCTATGATGCTGCAGTGGAGGGGG

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PEHQVAGHRASASKLGPLIDGSGLFYKPLQAGDRGEHE
PFPRFHGTRLLPTEAQPGEPHPYLVLDDLLAGFEAPCV
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                                                                                                                      CCCATAGTCCCCTTCCCCATACCATGTCCGACC
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                                                                                                 Gaps
                                                                                                 62;
                                                                          Length 899;
                                                                                                 40; Indels
                                                                          686; DB 6;
No. 7.5e-98;
matches 40;
8.1"
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Shi,J., Beach,L.R., Wang,H., Rafalski,J.A. and Cahoon,R.E. Novel inositol polyphosphate kinase genes and uses thereof Patent: WO 02059324-A 15 01-AUG-2002; PIONEER HI-BRED INTERNATIONAL, INC. (US) . Location/Qualifiers

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

sativa (japonica cultivar-group)"

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probably
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Direct Submission

Direct Submission

Submitted (18-SEP-2002) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(B-mail:tasaski@nias.affrc.go.jp, URL;http://rgp.dna.affrc.go.jp/,
Tel:81-299-38-7441, Fax:81-298-38-7488)

On Jun 28, 2004 this sequence version replaced gi:34740257.
Gens were predicted from the integrated results of the following:
GENSCAN (http://CRE-081.mit.edu/GENSCAN.html), FGENESH

(http://www.igr.org/tdb/glimmerm/glmt.form.html), RiceHMM

(http://www.igr.org/softdb/glimmerm/glmt.form.html), RiceHMM

(http://www.igr.org/softdb/glimmerm/glmt.form.html), RiceHMM

(http://www.igr.org/softdb/glimmerm/dlmt.form.html), RiceHMM

(http://bioinformatics.iastee.edu/cgi-bin/sp.cgi), sim4

BLASTN with the corresponding DBJ accession no.

A gene with identity or significant homology to a protein is

classified based on the protein name to indicate the homology (covering almost the entire length of partial as same name, butative-demulation program
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                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                   824 GGGGGCTCTGCTAGCTGATCAAGTTTGTTTCTGACATTGTTCCAGAGACTCCTTAGACG 883
GGCGGGCTCTGCTCGCTGATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCATACG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OSJNBa0047A17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Only in Database (2002)
2 (bases 1 to 149142)
Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP005749.3 GI:49388911
                                                                                                                                        901 CAGC 904
                                                                                                                                                                                                        CAGC 887
                                                                                                                                                                                                        884
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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AUTHORS
TITLE
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AP005749
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/product="putative ubiquinol-cytochrome c reductase
iron-sulfur subunit, mitochondrial precursor"
/protein id="BAD26134.1"
/db_xref="G1:49389912"
/translation="MLRVAGRELITALAWRPAAAGARGPLAGGSLPGDDEFSREPQR
PRFAVDSPFFAASRGFSSETLVPRNQDVSLTELPATVSAVKNPSAKIVYDEYNHERYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGDPSKRAFAYFVLSGGRFIYASLLRLLVLKFVLSMSASKDVLALASLEVDLSSIEPG
TTVTVKWRGKPVFIRRTEEDINLANSVDIGSLRDPQQDABRVKNPEWLVVIGVCTHL
GCIPLPNAGDFGGWFCPCHGSHYDISGRIRKGPAPYNLEVPTYSFLEENKLLIG"
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/gene="OSJNBa0047A17.6"
complement(join(18932. .19648,19740. .19836,20081. .20194,
20260. .20444,2069. .20827,20933. .20999,21093. .21207,
21277. .21382,21703. .21764,21859. .21993,22149. .22331,
22880. .22936,23369. .23417,23504. .23652,24724. .24771,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MENATVTAADLAPWSQQCRPVGEEEEGGVAAAAKKEEGRQIQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inactive due to including stop codon(s) in CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /going and properties by full-length cDNA(s): AK102815" complement (join(6112...675,8843...9017))
/gene="OSANBa0047h1.2"
/note="Reske iron-sulfur protein
contains EST(s): AU162272(C63256), AU068962(C51210)
contains full-length cDNA(s): AK102815"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<11599. .>12180)
/gene="OSJNBa0047A17.4"
/note="supported by full-length cDNA(s): AK109226"
complement(11599. .12180)
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/note="supported by full-length cDNA(8): AK120851"
                                                                                                                                                                                                                                                                          /note="hypothetical ORF
predicted by GENSCAN
this category is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            this category is not included in IRGSP standard" complement(18932. .25995)
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/gene="OSJNBa0047A17.3"
join(<9904. .10067,10732. .>10750)
/note="start and end point are not identified"
join(9904. .10067,10732. .10750)
/note="predicted by GENSCAN etc."
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/note="contains full-length cDNA(s): AK109226
non-coding transcript
                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join (5864. .6755, 8843. .9107))
/gene="OSJNBa0047A17.2"
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/gene="OSJNBa0047A17.5"
join(15870. .16043,16479. .16484)
/note="OSJNBa0047A17.5"
/note="hypothetical ORF
predicted by FGENESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
/protein_id="BAD26135.1"
/db_xref="G1:49388913"
                                                                                                                       /Clone="OSJNBa0047A17"
join(2637. 2780,3298. 3360)
/gene="OSJNBa0047A17.1"
join(2637. 2780,3298. 3360)
/gene="OSJNBa0047A17.1"
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                        complement (5864. .9107) /gene="OSJNBa0047A17.2"
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147160 TCCACCACCGCCGCCGCCGCCGCCGCCGCCATGGC--CTCCGACCTGCGCCCGCCG 147217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .29264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                        SWNARINVHYOPEVLOPIVFOVYDIDPOFHDVNEKMLKLEEQOFLGEAVCLLSEVITK
PURLLTLKLGVUSEHNLPNPSKFGELWOQAEESAGSKALMEWPRRSDLBIRDLLSKSD
PULLSRISESGVPPTCKTFKNDLMPKWRPVILMLQJIGSKENPLIIECPNFSSN
GKHDLLGKIVKSVABLEKMYHSODGENPFVPASTAHDSHSKEVLKSOVYVEKYLENNR
                                                                                                                                                                                                                                                                                                              QTFLDYISAGCQLNFMVAVDFTASNGNPRLPDSLHYIDPTGRPNAYQRALLEVGDVLO
YYLPDAKRFPSWGFGARPIDGPVSHCFRLNGSTYGDFUGGIQGTMAAY TABLRNVSLAG
PYLFGPVVSTATALANQQKYFVLLIYTDGVTDFQFTIDAIIKASDFLSIL
VVGVGGADFKEMEFLDPNKGERLESSTGRVASRDMIQPAPMKDAHGSGISTVQSLLAB
 COMPLEMENT (JOIN(19554. 19648,19740. 19836,20081. 20194, 20280. 20444,20690. 20827,20923. 20999,21093. 21207, 21277. 21382,21703. 21764,21859. 21993,22449. 22331, 22880. 22936,23369. 234771, 23569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oin(26913. .27610,27708. .29002,29099. .29157,29238.
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contains full-length cDNA(s): AK120851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="putative activator-like transposable element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 149142;
                                                                                                                                                                                                                                                                                                                                                                                                  complement(26424. .26747)
/gene="OSJNBa0047A17.7"
complement(join(<26424. .26494,26660. .>26747))
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gene="OSJNBa0047A17.9"
fnote="Betart and end point are not identified"
fgene="OSJNBa0047A17.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="start and end point are not identified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(26424]. .26494,26660. .26747))
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|oin(26913. 27610,27708. 29002,29099.
|gene="OSJNBa0047A17.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="predicted by GeneMark.hmm etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.7%; Score 546.4; DB 8; Best Local Similarity 77.5%; Pred. No. 3.1e-76; Matches 718; Conservative 0; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="predicted by GENSCAN etc."
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gene="OSJNBa0047A17.9"
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                                                                         . .25746))
                                                                                                                                           codon start=1
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chromosome 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147698 eccesesárces cecesar ecreces estas 
certicaceacacccerticifcicesecccaecaccceeceecececcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147638 GATGCCCGGGGCGCGCGTGTGGCGCCCGGACCGGTCGGAGCTGAAGGGGATCGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147758 recececriceccecececereraceaaceeaacecececerereceaececeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGCGGGCTCTGCTCGTTCATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCAT
                                                                                                                                                                                                                                                                                                                                                                                       TACGCCGCGTTCACCGCGCACCCGGCCGTCCCGCCCCGGGTCCGGGCGCCTTCTTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCAAGGCGTGGTTCGAGGAGCAGACTCTGTTCCACTTCTACTCGGCGTCGATTCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147878 Gectaceaceceaarecedededededececerecrecedaderedaagecegeretaage
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                                                                                                                                                                                                                                                                                                                                 TATGAGGCGTTCTCCGCCCACGCCGCCGTCCCGGCCCGCATCCGAGACACCTTCTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCTCGTCCTCGACGACCTCCTCGCGGGGTTTCAGGCGCCCTGCGTCGCAGACATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 ATCGGCGCATCACGTGGCCACCGAGTTCGCCGGAGCCCTACATCGCCAAGTGCCTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGACCGCGGGACCACGAGCGTTCTGCTCGGATTCCGCGTCTCCGGCGTCCGAGTCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGCCGTCCGCCGTGCTCCGGCGCTACGTGTCATCCGTTGCCGACGAGGGGATGGAC
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                                                                                                                                     133 TCCGGCCTCTTCTACAAGCCGCTCCAGGCCGCCGACCGTGGGGAGCACGAGGTCGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGTTCCACGGCACGCGACTCCTCCCCACCGAGGCGCAGCC---CGGGGAGCCGCATCCT
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PAC clone:P0415B12.
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Oryza sativa (japonica cultivar-group)
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KEYWORDS
SOURCE
ORGANISM
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13 TCGTCACCCTCGCGCCCATAGTCCCCTTCCCCATACCATGTCCGACCTCCACCGGCGG

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IRKSIFCDROSSGTIPCOTLGSTYPPRIDGTDXFGFGPPDBSERIRGBDRRTLEALY
TFPTLLPCVNENVPLSEILEDCROSTLASRALKFIGSMSLAPDELQFVGIIGDSDRRTLEALY
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/kwri.ps.as.ps.ara.ps.ala.strvx.ps.ala.strvk.appil.ss.ps.as.ps.ara.ps.as.ps.ala.strvx.appil.ss.ps.as.ps.ala.strv.appil.ss.ps.as.ps.ala.strv.appil.ss.ps.as.ps.ala.strv.appil.ss.ps.as.ps.ala.strv.appil.ss.ps.as.ps.ala.strv.appil.ss.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.ps.as.
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complement(join(16881. 17069,17267. 17644,18400. 18594,
18674. 18751,18816. 19001,19077. 19307,19386. 19739,
1937. 20034,20118. 20288,20405. 20512,20611. 20829,
20914. 21120,21227. 21445,21564. 21638,21998. 22150))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (join(8929. .9060,9161. .9334,9438. .9569,
9640. .9738,9929. 10000,10080. .10136,10206. .10379,
10460. .10554,10727. .10826,10921. .11073,11145. .12275,
12870. .12980,13078. .13240,13613. .13707,13793. .14053,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (join(8669. .9060,9161. .9334,9438. .9569,
9640. .9738,9929. .10000,10080. .10136,10206. .10379,
10460. .10554,10727. .10826,10921. .11073,11145. .12275,
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14178. .14331,14775. .15038)
/note="supported by full-length cDNA(8): AK121782"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="P0415B12.3"
/note="contains EST(8): AU082722(R4038),AU032417(R4038)
contains full-length cDNA(8): AK121782"
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                                       /hote="start and end point are not identified"
join(6055..607,6830..7404)
mome="polsb12.2"
/note="predicted by FGENESH etc."
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/protein_id="BAD25376.1"
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/gene="P0415B12.4"
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Direct Submission

Direct Submission

Submitted (30-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Ric Genome Research Program; Kannondai (21-21-27 Tsukuba, Idearki 305-6802, Japan to February Sciences, False Genome Research Program; Kannondai (E-mail:teasakienias.affrc.go.jp, URL:http://rgp.dan.affrc.go.jp, GeneWark.hum

(http://www.tigr.org/tackydinmerm/glmr.form.html), RiceHWM

(http://rgp.dan.affrc.go.jp.RiceHWM/), SplicePredictor

(http://rgp.dan.affrc.go.jp.RiceHWM/), SplicePredictor

(http://globin.cse.psu.edu/html/docs/sim4.html), gap2

(http://grobin.cse.psu.edu/html/docs/sim4.html), gap2

(http://grobin.cse.psu.edu/html/docs/sim4.html), gap2

regions ware searched against NCB1 NonRedundant Protein Gapsen with the corresponding DBJ accession no.

Pull-length Dasse at Regp or DDBJ accession no.

Rudiction of the protein programs is also classified as a hypothetical protein accediction progra
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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/gene="P0415B12.1"
/note="supported by full-length cDNA(s): AK121467"
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Moul type="genomic DNA"
(cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0415B12
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/gene="contains full-length cDNA(s): AK121467
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join(<6065. .6067,6850. .>7404)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                    Published Only in Database (2002)
2 (bases 1 to 157419)
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/gene="P0415B12.1"
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/clone="P0415B12"
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satch,K., Nagata,T., Kawagashira,N., Doi,K., Kikhuchi,S., Satch,Y., Jahikawa,M. Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahadi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Islayiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Matsubara,K., Riken,,K., Ishibiki,J., Kawamata,M., Matsubara,K., Riken,,K., Habildume,W., Hayatsu,M., Imota,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hasyatum,M., Imota,J., Carninci,P., Adachi,J., Aizawa,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Myazaki,A., Osaato,N., Ota,Y., Saito,R., Shikaki,T., Saito,R., Shikaki,T.,
10186 CACATCGTCCTCGACGACCTCCTCGCGGGCCTCCCGTCCCCCTGCGTCGCCGACGTCAAG 40245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10666 greaagcriegregacriregegerargregacgargacgaggaggargarreaccacaacric 40725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crcaaggcgrggrrcgaggaggaaaccrgraccacrrcracrcggcgrcgarrcrgrrc 40605
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AK072296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK072296.1 GI:32982319
PLI CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                          eccesestrcscccccarecrcscccccracererccacesccsccsccacesccace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10606 GECTACGACGCCAATGCGGCGGCGGCGCTCCTCCCGGAGGTGGAAGCGGCGGTGTAAGG
                                                                                                                                                                                                                                                                                                                                                             ---GGCCCCGAGGCGCCGTGTGGCGGACGGAGGCCCCGGAGGTGAAGGCCATGGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 CTGGGCGGGCTCTGCTCGCTGATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCAT
                                                                                                                                                                                                                 AAGGACCGCGGGACCACGAGCGTTCTGCTCGGATTCCGCGTCTCCGGCGTCCGAGTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCGGCGTCCGCCGTGCTCCGGCGCTACGTGTCATCCGTTGCCGACGAGGGGATGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGCGCTCGCCGCGGCGGTGTACGGAGGAAAAGGTGGAGTCTTGTCACACCAGCTGCGCGAG
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YLMAPRLARRGGVDEPPAWESREFLERKLCIGKEVTFRVDYTAPNVGREFGTYVLGDKN
VAYSITAAGWARVKEGGFRGGEPSPYLTELLELBEVAKQGGLGRWSKEPGAAEESIRD
LPPSAJGEASGFDAKGFAVANKGKSLEAIVEGVRDGSTVRYVLLIPSFOFVQITVAGVO
SPSMGRRPPPNPTVVAAAESTADGATNGGDSEEAPAPLTTAQRLAAAAVSTEIPPDRFG
IRAHFFFRIVLINRDVAIVVEGTDSFSNIIGSYYXSOGOTLKDLALELVENGLAKYVE
WSAMMDVDAAKIKLKNABLQAKKDQLATNTAGREPRPPTNSKPIHDQKFTGKVVEVVSGD
CIIVADDAAPYGSPSARRVNLSSIRAPKMGNPRRDEKKDNFAREAKEFLRFGY
VTVEMBYSRRISTVORGPTTNTADARVLDKSPRONDSSIPSGODGGT
                                                                                                                                                                                                                                                                                                                                                      NIAETLLSRGFARTSKHRDYEERSHYFDLLLAAESRAEKÄKKGVHSAKESPVMHITDL
TYSAKKARDFLPFLQRNRHSALVEVPGGHRFKLITREKTGSLAFSFGGRAFDEKD
TPYSAKBAIALMRRILLQRDVEIEVBAVDRTGFLGSLWESKTWMASVLLLEAGLAKLSS
FGLDRIPDANVLMRAEQSAKQQKLKIWENYVEGEEVSNGSASESKQKEILKVVVTEVL
GOGKFYVQYCHRWASQDROCHSKLKADAVIGAFNDVKGETVLAQFSTAGSADNGWNRAM
IVNGRRGAVSGQDREVFYIDYGOGLASLIKADAVIGAFNDVKGETVLAQFSADNGWNRAM
TVNGRRGAVSGQDREVFYIDYGONGWYPSRIRPADDSISSSPALAQLCAFIKV
PNLEDDFGHBAAVYLNDCLLNSQKQYRAMIEERDTSGGGKSKGQGTILIVTLVDAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETSINATMLEEGLARLERSKRWDTRERKAALQNLEQFQEKAKKERLQIWQYGDVESDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGAGGCGTTCTCCGCCCACGCCGCCGCTCCCGCATCCGAGACACCTTCTTCCCC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGTTCCACGGCACGCGACTCCTCCCCACCGAGGCGCAGCC---CGGGGAGCCGCATCCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCTCGTCCTCGACGACCTCCTCGCGGGGTTTCAGGCGCCCTGCGTCGCAGACATCAAG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0415B12.7"
/note="Bimilar to Oryza Bativa chromosome7, P0404G11.101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probably inactive due to including stop codon(s) in CDS pseudogene, TNP2" /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 TCCGGCCTCTTCTACAAGCCGCTCCAGGCCGGCGACCGTGGGGAGCACGAGGTCGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 TCCGTCACCCCTCGCGCCCATAGTCCCCTTCCCCATACCATGTCCGACCTCCACCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted by GENSCAN
this category is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 157419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (31727. .32496)
/gene="P0415B12.7"
complement (join (33727. .32242,32434. .>32496))
/gene="P0415B12.7"
/note="gtart and end point are not identified"
complement (join (31727. .32242,32434. .32496))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(25322. .25357,28498. .28641)

gene="p0415B12.5"

101n(25322. .25357,28498. .28641)

gene="p0415B12.5"

/note="hypothetical ORF
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Pred. No. 3.1e-76;
0; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein_id="BAD25377.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29565. .3<u>1</u>528
/gene="P0415B12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="P0415B12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEQAPAARRTGGRR"
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Best Local Similarity 77.5
Matches 718; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAIGAGGCGIITCICCGCCCACGCCGCCGICCCGGCCCGCAICCGAGACACCTICITCCCC 252
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        Mismatches 192; Indels
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2 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayashizaki, Y., Itaha, Y., Itaha, T., Tohibiki, J., Ishikawa, M., Itoh, M., Kaqawa, T., Kanagawa, S., Katoh, H., Kawagashira, N., Kawan, J., Kawamata, M., Kanagawa, S., Katoh, H., Kaugashira, Y., Kodama, T., Kojima, Y., Kojima, Y., Konda, S., Konno, H., Kouda, M., Kodama, T., Kojima, K., Kojima, Y., Kojima, S., Konno, H., Kouda, M., Masuda, H., Matsubara, K., Murata, T., Muina, J., Miyazaki, A., Masuda, H., Matsubara, R., Murata, T., Makamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Shinagawa, A., Shiraki, T., Salaki, T., Sogabe, Y., Sugano, S., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Suzuki, K., Suzuki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Falls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fulimura,T. Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodamata,T., Kucosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanamata,Y., Arakawa,T., Carninci,P., Fukuda,S., Hanamata,Y., Hara,A., Hashiuume,W., Hayatsu,M., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kanagawa,J., Kanagawa,S., Kacho,H., Kawai,J., Kanagawa,J., Kanagawa,J., Kondo,S., Konno,H., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
Yamamoto, M.
                                                    over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is one of the 28K full-length cDNA clones from japonica
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Pred. No. 9e-76;
                                                    늉
                                               Collection, mapping, and annotation japonica rice
                                                                                                                                       ence 301 (5631), 376-379 (2003)
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J023018G11"
                 foshino, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.5%;
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Best Local Similarity
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TITLE JOURNAL

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PAT 05-OCT-2002

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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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  and uses thereof
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Pred. No. 2.1e-20;
0; Mismatches 21;
Novel inositol polyphosphate kinase genes Patent: WO 02059324-A 18 01-AUG-2002; PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                          Score 298.4; DB 6;
Pred. No. 3.8e-37;
0; Mismatches 38;
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Shi,J., Beach,L.R., Wang,H., Rafalski,J.A. and Cahoon,R.E. Novel inositol polyphosphate kinase genes and uses thereof Patent: WO 02053324-A 17 01-AUG-2002;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Submitted (22-MAR-2001) Dodds P.N., Plant Industry, CSIRO, GPO 1600, Canberra, ACT 2601, Australia
Location/Qualifiers
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    ^organis="Bucalyptus grandis"
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/gene="Ngc-A"
join(12668. 13218,13450. 14542,14757. 15032,15186. 16493)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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/tb_xref="Uniproot/TrEMBL:09ARC3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGSRTWYPBASQAYIEKCLKKDVESSPFLGFRISGLQVYGNDKESSEVVLKPERKLL
QNLTADEVRLVLKRFVSSNPKSDQPDCSFAAVVYGGSNGILAQLLELKAWFEDQTIYH
FNSCSVLMLYEKEKTKMVNGGEESLGCAAVKLIDFAHVTEGNGVIDHNPLGGLCSLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LÓELAKOVGCWKSGGGAKGQHILLPVFLFVDPRDVRHTESGSYKEAFEEHSQKHDPET
VLEWREALGGYGEMKGTHYTESDGHGSIDKLITEVELHLIGANYALVPDELVGIDSRV
DEVVGLINLDSSYSEKIIGTHGMGGLGKTTLAKAVDRYSTKFERCYFLENIRDTLSE
KNGVSILQNKIISGILKKDFNEAKNASDGIRIIRDRYCRHKLLIVLDDVDEKFQFDDV
LGKLNNFSTRSRFLITTRDARGLELLOSYKMFELGENGSPSPHSTLTRRYARFDVCDPK
DAYLLSKEFVQAAGLDLYIKVIGSLLERMDKIFWERGLEBFKKISPTKVGPRIKISY
NELTHNEKQIFLDIACYFIGSQKIYPIPMWEDCDFYPESTIRSLIQKSLIKLOSKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDVLNTFWMHDHIDLGRAIVREEKNQNPYKRSRIWSNKDAVNMLKHKKGTDČVEVLJT
VDMGESBLILTNKREFEKLTHAKYLKYSNRALADDFKDVLDANLRALLLESSCDSVPSGLY
LKKLVRLDLADCSOSWKGWNELKVARKLKAVSLKRCFHLKKVPDFSDCGDLEFELNF
DGCRNMRGEVDIGNFKSLRFLYISKTKITKIKGEIGRLLNLKYLSVGDSSLKEVPAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKLSSLEFLALALTDSYKSDFTEMLFTSLTLLYISNDTQKFCPDTSSENLQRLPNLSN
INISSVLYLIDVGGETGGELGAGELANETYLSIGSASRINHIDGEBNULJUHLRYBGCR
ILRKLPSLJALTRLQUCPLWIDQCPLVTEINGMQLWESLSHLKVVGCSALIGLSSLHSM
VKLERLLLVGCVLTETWPPSLSMFTKLTELSLCAMPWKQFPDLSNLKNLRVLCMSFCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cranslation="MMRSDSNGSTDSFHSCSSADLTFPPLPSGEYEVFLSFRGPDVRK
TFADHLYTSLVRSKFRTFRDEEELEKGGTIGPSLIRAITESKIYIPILTPNYASSKWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELIEVPGLDALESLKWLSMEGCRSIRKVPDLSGLKKLKTLDVESCIQLKEVRGLERLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name="n-X50"
/note="&le of 11 bp insertion in n-X50 rust susceptible
mutant allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name="n-X128A"
/note="SiTe of LUTE transposon insertion in n-X128A rust
susceptible mutant allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'standard name="n-X139"
note="233 bp deletion in n-X139 rust susceptible mutant
                                                                                                                        join(2881. .3431,3533. .4652,4770. .5045,5140. .6519)
|gene="Ngc-D"
                                                                                                                                                                                                        join(2881. .3431,3533. .4652,4770. .5045,5140. .6519)
gene="Ngc-D"
                                                                                                                                                                                                                                                                                    note="N rust resistance gene: TIR-NBS-LRR protein"
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organism="Linum usitatissimum"
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                                                                                                                                                                                                                                                                                                                                   /product="Ngc-D protein"
/protein id="CAC35321.1"
/db xref="G1:13509207"
                              'mol type="genomic.DNA"
'variety="Bombay"
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                                                                                          xref="taxon:4006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 _xref="GOA:Q9ARC4"
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/function="unknown"
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join(20265. .20815,21104. .22202,22415. .22690,22818. .24218)
|gene="Ngc-B"
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GELDIGTFKDLKVLDINQTEITTLKGEVESLQNLQQLDVGRSGLIEVPAGISKLSSLE
ELDFLSKVHDDEVEMLENGSLELLVISSESLALDPSELIKLDICOSRNLQRLPNLASVTN
LTRLHKEVGIHEIPGGLKKKLLESLSICNPNLDNLDGLENLVLKELALERCPILG
KLPSLAELTKLHKVVIRWCDVLGEIYGLOGDSLSHLDISWCPRLTVMDLLHSLLKL
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MHDHIRDLGRAIVCEESQNLYKRSRIWSNNDAIDILKKNREGNDCVEALRVDMRGEGFA
LTNEEFKQFSRLRFLEVLNGDLSGNFKNVLPSLRWLRVYHGDPCPSGLNLNKLMILEL
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| Translate.ion="MikvpEHQVAGHQDINGLIGDEVDDSGRFYKPLQCDERGATEMA
| FYTSFSTRKTIPQYKRFFQAFQGTQSIBASDGSGLHPHLILEDLTSTRLHLCVMDIK
| IGSRTWYPBASQAYIEKCLKKUVESSNPLLGFRISGLQVYGNGKESSEVVLKPERKLL
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FNSCSVLMLYEKEKTKMVNGGEESLGGAAVKLJDFAHVTEGNGVIDHNFLGGLCSLIK
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NELTHNEKQIFLDIACLFVGAKKEVPMYMWSDCDLYPASTLRTLVQRSLVRMDDNKKF
WHHDHIRDLGRTIVREENSQNPYKRSRIWSNNDAIDILKNREGNDCVEALRVDMKGEG
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LQELAKWYNCWKNGGEAKGQHIIIPVFYFWDPRDYRHPDSGEYKESFEQHNLKHDPFT
ILBWKGALQBYGKGKKKKWHISELTGQGAVVDKIFTEVELHLRANYTLATDELVGIDFSV
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DGVVALQNKYISDILRKDFCQAKNASDGVQMTRERVSHKHFTVVLDDVNBSFRFDDIF
GKLTAFSADSRFLVTTRELRGCKLFRHEGMSHDHSIKLFSKHAFGVDYPPED
YASLCEBFYQVGSGIPTDAATLERIRGCKFFRHEGMSHDHSIKLFSKHAFGVDYPPED
YASLCEBFYQVGSGIPTDAALKVIGSLIPRTEKSFWKDKLIELKAIPAVNVQYRLKISYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVSDVTDSWEGWNEIKAAGKLKVVHLMCCKGLEKVPDLSTCRGLELLRFSICRRMIGE
LIDINKFOLDLKVLDI RQTRITALKGEVRSLQNLQQDVGSSGLI EVPAGI SKLSSLEYL
ILTINIKHDKVETLPRGLKILLI SESFSLAALPSSLFRLDVRYSTNLRRLPNLASVTNLT
RLRLEBVGIHGI PGLGELKLLECLFLRDAPNLDNLDGLENLVLLKELAVERCRILEKL
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ELEGGYGTIYNLLPPSLSIYTKLKSLKVYSDSQUDEDTNIKNKTRCLKIGGCDNFIETTGL
HTLESLEELRVMGSSIKLDLTGLYKLEILOPDSCTQLTEIRGLGGLESLQRLHMSRC
QSIKELPNLSGLKILSYIILEKCRHLKEVYRLEELKRLDFNTHRG"
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/gene="Ngc-B"
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rust resistance gene homolog: TIR-NBS-LRR
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/db_xref="UniProt/TrEMBL:Q9AR40"
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/db_xref="GI:13509210"
                                                                                                                                                                         /product="Ngc-A protein"
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/db_xref="G1:13509209"
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/function="unknown"
                                                                                                                       codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9958
GTLVSSGFELTNILPLSLSIYTKLRTLEVRSSQLPDLTNLKNLRDLTITGCRELIEIA
GLTLESEBELSMERCPSVRKLDLAGLIKLKTTHIHICTQLTETRGLGGLESLQNLFM
SGCOSIKELPNLSGLXKLKYFSLKECRQLKEVNGLEELEWLDFNTDRRLKLKYLKLKJ
SRKGKQLVTQSARRALFINN"
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RESULT 15 AX513572

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DVKIGSRTWHLGDSEDYICKCLKKDRESSSLPLGFRISGVKDSISSWEPTRKSLQCLS
ANGVALVINKFVSSNNINHDDHHPDGAFATEYYGAVLERLQRLKDFRISGVCS
SVLVYYFKDLGKGKATNPLVKLVDFAHVVDGNGVIDHNFLGGLCSFIKFLKDILAVAC
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             652 TCACAGCTGCGCGAGCTCAAGGCGTGGTTCGAGGAGCAGACTCTGTTCCACTTCTACTCG 711
                                           603 GAGGCTTGCAGAAGCTCAAGGACTGGTTCGAGGTTCAGACGTGTATCACTTCTATTCT 662
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Sequence 17, Appl Sequence 4649, Ap Sequence 18, Appl Sequence 10743, A Sequence 19, Appl Sequence 11, Appl

Title: Perfect score:

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Scoring table:

Searched:

Database

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US-10-042-894A-7

Sequence 7, Application US/10042894A

Publication No. US20030009011A1

GENERAL INFORMATION:

APPLICANT: Bacch, Larry

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

TITLE OF INVENTION: Genes and Uses Thereof

FILE REFRENCE: 1202-01-09

FRICK PRING DATE: 2002-01-09

PRIOR PILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO 7

LENGTHEN: 1344
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0. 1284 15 US-10-139-963-1189

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Pred. No. 0;
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Sequence 74436, A
                                                                                                                                                                                                            June 17, 2005, 00:32:13 ; Search time 879 Seconds (without alignments) 9491.401 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-425-115-74438
US-10-042-894A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6054689 seqs, 3103772919 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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1307 865.4 844.8 837.4 740.4

Score

Result Š.

Sequence 15, Appl Sequence 1, Appli

Sequence 10.467, Sequence 11.4 Appli Sequence 13.4 Appli Sequence 14.4 Appli Sequence 1.7 Appli Sequence 1.7 Appli Sequence 1.7 Appli Sequence 57529, A Sequence 2855, A Appli Sequence 1180, Appli Sequence 1180, Appli Sequence 1266, Appli Sequence 13130, Sequence 1315, A Sequence 2726, Appli Sequence 1315, A Sequence 1315, A Sequence 1189, Appli Sequence 1189, Appl

GENERAL INFORMATION:  APPLICANT: Shi, Jinrui APPLICANT: Beach, Larry APPLICANT: Wang, Hongyu APPLICANT: Wang, Hongyu APPLICANT: Cahoon, Rebecca E. TITLE OF INVENTION: No. US20030009011A1el Inositol Polyphosphate Kinase TITLE OF INVENTION: Genes and Uses Thereof FILE REPERENCE: 1286 CURRENT APPLICATION NUMBER: US/10/042,894A CURRENT FILING DATE: 2002-01-09 FRIOR PILING DATE: 2001-01-12 NUMBER OF SKO ID NOS: 37 SOFTWARE: FastSKO for Windows Version 4.0 SEQ ID NO 5 LENGTH: 923 TYPE: DNA ORGANISM: Zea mays FRATURE: NAME/KEY: CDS LOCATION: (53)(922) US-10-042-894A-5	Query Match 64.4%; Score 865.4; DB 14; Length 923; Best Local Similarity 98.8%; Pred. No. 2.8e-236; Matches 870; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Ov 42 TCCCGATACCATGTCCGACGTCCACGCGGAGGACCAAGTCGCCGGCCACCACGCCGCGCAAGTCGCCACCCCACGCCGCGCAAGTCGCCACCACGTC 101	102 CGCCAGCAGCCCGCCGCCCGCCGGAGCTCTTCTACAAGCCGCTCCTCTCTACAAGCCGCTCCTCTCTACAAGCCGCTCCTCTCTACAAGCCGCTCCTCTCTACAAGCCGCTCTCTCT	162		283 CGAGGCGCAGCAGCAGCACCTCGTCTCGACGACGACCTCCGCGGGATT 342 TCAGGCGCCTGCGTGCAGACATCAAGATCGGCGCCTCCTCGACGACGACGACGACGATTGGCC 343 TCAGGCGCCTGCGTGCAGACATCAAGATCGGCGCCATCACGAGGTTCGCC 343 TGAGGCGCCTGCGAGACATCAAGATCGGCGCCATCACGTGGCCACCGAGTTCGCC	Qy         402 GGAGCCTACATCGCCAAGTGCCTCGCCAAGGACCGCGGGACCACGAGCGTTCTGCTCGG 461	Qy         462 ATTCCGGGGTCCCGAGTCGTCGGCCCCGAGGGCGCCGTGTGGGGGCGCGTGTGGGGGGGG	Qy         522         CCCGGAGGTGAAGGCCATGGACACCGCCGGCGTCCCGCCGCGTGCTCCGGCGTGTC         581           Db         523         CCCGGAGGTGAAGGCCATGGACACCGCCGGCGTGCCGCGCGTGCTCCGCCGCTGTC         582	Oy 582 ATCCGTTGCCGACGAGGGATGGACTGTGCCGCTCGCGGGGGGTGTACGGAGGAAAAGG 641	Qy         642 TGGAGTCTTGTCACAGCGGAGGTCAAGCGTGGTTCGAGGAGCAGACTCTGTTCCA         701           L
368 AGATCGGCGCCATCACGTGGCCACCGAGGTTCGCCGAGGCCCTACATCGCCCAAGTGCCTCG 436 AGATCGGCGCCATCACGTGGCCCACCGAGTTCGCCGAGGCCCTACATCGCCCAAGTGCCTCG 436 AGATCGGCGCATCACGTGGCCACCGAGTTCGCCGGGCCTCTCGCCAAGTGCCTCG 495 CCAAGGACCGCGGGACCACGAGCGTTCTGCTCGGATTCCGCGTCTCCGGCGTCCGAGTGG 496 CCAAGGACCGCGGGACCACGAGCGTTCTGCTCGGATTCCGCGTCTCCGAGTCG 497 TCGGCCCCGAGGCGCTGTGGCGGACTTCTGCTCGGGTTCCGGTTCCGAGTCG 497 TCGGCCCCGAGGCGCGTGTGGCGGAGCTCTCGCGTTCCGGTTCCGAGTGGACCG 498 TCGGCCCCGAGGCGCTGTGGCGGAGCTCTCGCGTTGGCGGGTTCCGATGGACCG 497 TCGGCCCCGAGGGCCCTGTGGCGGAGCGCCCGGAGGTTCCGGTTGCCGAGGGATCGACCG 498 TCGGCCCCGGGGCTCCGGCGCTTCGGTTCCGTTGCCGAGGGGATGGACCG 497 TCGGCCCCCGAGGCCCGGGGCTACGTTCTCGGTTGCCGAGGGATGGACCG 498 TCGGCCTCCGCCGGCGCTTCCGGTGCTTCCGTTGCCGAGGGATGGACCG 497 TCGGCCCCCGGGGGCCGTGCTCCGTTGCCGAGGGATGGACCG 498 TCGGCTCCGCCGGGGGTTCCGGGGGGATGGACCGGGGATGGACCGGGGATGGACCGGGGATGGACCGGGGGATGGACCGGGGGATGGACCGGGGGATGGACCGGGGGATGGACCGGGGGATCCGTTGCCGAGGGAGG	728 GCTATGATGCTGCAGTCGCAGCAGAGAGATGGGGGTGGGGTGACGGTGACGGTGAGGTGG 787	155 TGGACTTTGCCCATGTGGCCGAGGGTGATTGACCACAACTTCGGGCGGG	B TGGGTCCTTCTTAAGAGAATCCTGGCATTTCGATTTGATAACAAAGCCCTACAAGTTT	OY 968 TGTCTGGAAAAGAAGCCCCTCCGAGTTGTGCTGGGGTGGAGATCTGAGACGGTCGTCG 1027	1095 GCCACTTGCTTGCCTTGCCTTGCCTGCAACATACGGCAACCTGCTCTTTTT 1088 TCGCAACCCCTTACTTCCGAAGAACTTTTTTTTCCCACTTTGGGGGTTCGATTACGTT 1155 TCGCAACCCCTTACTTCCGAAGAACTTTTTTTTCCCACTTTGGGGGTTCGATTACGTT 1155 TCGCAACCCCTTACTTCCGAAGAACTTTTTTTTTCCCACTTTGGGGGTTCGATTACGTT	1148 GGATCTGGTTTGTGCCACTCGGTCAGAGGTTGTAAGCATGGAGGGAG	Oy 1208 GCAACTGTGAGTCTTTGCGCTGCCGTTTCTGCATGGCTTTTGCCTGCTGCGATC 1267	OY 1268 CGATGTGTACTGGAGATGGTGATGGACGTCTCTACCTCCAAAGGAATCGTCCGATA 1327	1328 AAAAAAA 1334          1395 AATCTAA 1401	RESULT 3 US-10-042-894A-5 ; Sequence 5, Application US/10042894A ; Publication No. US20030009011A1

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Sequence 3, Application US/10042894A;
Sequence 3, Application US/10042894A;
Publication No. US2003009011A1
GENERAL INFORMATION:
APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Genes and Uses Thereof;
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09;
PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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62.3%; Score 837.4; DB 14; Length
Best Local Similarity 97.5%; Pred. No. 2.7e-228;
Matches 859; Conservative 0; Mismatches 21; Indels
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; LOCATION: (53)...(736)
US-10-042-894A-3
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ORGANISM: Zea mays
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US-10-042-894A-3
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Sequence 1, Application US/10042894A

Publication No. US2003009011A1

GENERAL INFORMATION:

APPLICANT: Back, Jinrui

APPLICANT: Back, Larry

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

TITLE OF INVENTION: Rebecca E.

TITLE OF INVENTION: Genes and Uses Thereof

TITLE OF INVENTION: Genes and Uses Thereof

TITLE OF INVENTION: Genes and Uses Thereof

TITLE OF INVENTION WIMBER: US/10/042,894A

CURRENT FILING DATE: 2002-01-09

PRIOR PILING DATE: 2002-01-09

PRIOR PILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 37

SEQ ID NOS: 37

SEQ ID NOS: 37

INVENTIOR OF SEQ ID Windows Version 4.0
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                                                                TGGGGGTGGGGTGACGGTGAAGCTGGTGGACTTTGCCCCATGTGGCCGAGGGTGATGGGGGT
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; LOCATION: (84)...(806)
US-10-042-894A-1
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Best Local Similarity
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ORGANISM: Zea mays
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CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PARESEQ for Windows Version 4.0
LENGTH: 3416
                                                                                                                                                                                                                                                      Best Local Similarity 90.23
Matches 862; Conservative
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                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (72)
US-10-042-894A-20
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Publication No. US20030009011A1

GENERAL INFORMATION:
APPLICANT: Shi, Jinrui
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca B.
TITLE OF INVENTION: No. US2003009011A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
FILE REFERENCE: 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCCG-TTGCCGACGAGGGATGGACTGTGCGCTCGCCGCGGCGGTGTACGGAGGAAAAG
                                                  CGCCAGCAAGCTGGGCCCGCTCATCGACGGCTCCGGCCTCTTCTACAAGCCGCTCCAGGC
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                                                                                                                CGGCGACCGTGGGGAGGACGACGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCCGT
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US-10-042-894A-20
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TCGGTCAGAGGTTGTAAGCATGGAGGGAGGCGTGTTGATCCGGCAACTGTGTCAGTCTTT 1225
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APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Beach, Larry
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: No. US2003000911A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR PLING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15.
                                                                                                                             676 TCGGTCAGAGGTTGTAAGCATGGATGGAGGCGTGTTGATCCGGCAACTGTGTCAGTCTTT 735
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                                          2 CACGAGGTCAGTCCGTCACCCCTCGCGCCCATAGTCCCCTTCCCCCATACCATGTCCGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 686; DB 14; Length 899;
Pred. No. 4e-185;
0; Mismatches 40; Indels 6
                                                                                                                                                                                                                                                                                  1226 GCGCTGCCTGTTTCTGCATGCTTTTGCCTGCTGCGAT 1266
                                                                                                                                                                                                                                                                                                        GCGCTGCCTTTCTGCATGGCTTTTGCCTGCTGCGAT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 15, Application US/10042894A; Publication No. US20030009011A1; GENERAL INFORMATION:
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Best Local Similarity
Matches 802; Conserv
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ORGANISM: Zea mays
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; NAME/KEY: CDS
; LOCATION: (89).
US-10-042-894A-15
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                                                                                                                                                                                                                                                                         Sequence 74436, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongeic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERBURS: 38-215322JB
CURRENT APPLICATON UNMBER: US/10/425,115
CURRENT APPLICATION UNMBER: 2003-04-28
CURRENT PILING DATE: 2003-04-28
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                                      841 GGCGGGCTCTGCTCGTTGATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCATACG 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 TGTACGGAGGAAAAGGTGGAGTCTTGTCACAGCTGCGCGAGCTCAAGGCGTGGTTCGAGG 196
                                                                                807 GGCGGGCTCTGCTAGCTGATCAAGTTTGTTTCTGACATTCTTCCAGAGACTCCTCAGACG
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                                                                                                                                                    867 CAGCCTTTGGGTCCTTCTTAAGAGAGGATCCTGGCATTTTCGATTTGATAACAAAG 922
                                                                                                                           901 CAGCCTTTGGGTCCTTCTTAAGAGGATCCTGGCA-TTTCGATTTGATAACAAAG 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.1%; Score 687.4; DB 20; Length 776; Best Local Similarity 99.7%; Pred. No. 1.6e-185; Matches 699; Conservative 0; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               566 recedentacenenearcerrecerreceaegaegargeaege
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OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: ungure
LOCATION: (1)..(
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US-10-042-894A-17
Sequence 17, Application US/10042894A
Sequence 17, Application VO. US20030009011A1
GENERAL INFORMATION:
APPLICANT: Shi, Larry
APPLICANT: Wang, Hongyu
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: No. US20030009011A1e1 Inositol Polyphosphate Kinase;
TITLE OF INVENTION: Genes and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                          367 GTCGCCAAGTGCCTCGCCAAGGACCGCGAGACCACCACCAGCGCGCTCCTCGGCTTCCGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                            187 CGGGGCGCTTCTTCCCGCGCTTCCACGCTTCCTCCCGGCCCCAGCCCCC
                                                                                                                                                                                                                                       247 GGGGGGGGCCCTACCCGCACATCGTCCTCGACGACCTCCTGGGGGCCTCCCGTCCCCC
                                                                                                                                                                                                                                                                                                                                      412 ATCGCCAAGTGCCTCGCCAAGGACCGCGGACCACGAGCGTTCTGCTCGGATTCCGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487 CTGAAGGGGATCGACGCCGCCGGGGTCCGCCGCTGCTCCGCCGCTACGTGTCCACGGGC
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                7 TCCGACCTGCCCCGCCCGAGCACCAGGTGGCGGGGCACCGCGCCGCCGCCGAACTG
                                                     GGCCCGCTCATCGACGGCTCCTCTTCTACAAGCCGCTCCAGGCCGGCGACCGTGGG
                                                                    175 GAGCACGAGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCCGCCCGGCCCGCATC
                                                                                                                             127 GAGCACGGCCTTCTACGCCGCGTTCACCGCGCACCCGGCCGTCCCGCCCCCGGGTC
                                                                                                                                                                235 cgagacacerrerrececegerrecaegeaegeaegeaerececeaegegegeaegee
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APPLICANT: La Rosa, Thomas J.
APPLICANT: APOLIC, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 4650
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40.6%; Score 545.6; DB 19;
Best Local Similarity 78.6%; Pred. No. 4.7e-145;
Matches 695; Conservative 0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_11514C.1
US-10-437-963-4650
                             399 ACATCAAGATCGGTGCCATCACGT-----
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ORGANISM: Oryza sativa
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                                                                                                                                                                                                      Score 308; DB 19; Length 6
Pred. No. 2.4e-77;
0; Mismatches 185; Indels
                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_11513C.1
US-10-437-963-4649
     FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF ESQ ID NOS: 204966
SEQ ID NO 4649
LENGTH: 696
                                                                                                                                                                                                      Query Match 22.9%;
Best Local Similarity 69.6%;
Matches 451; Conservative (
                                                                                                       TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
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US-10-042-894A-18
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thous APPLICANT: Stou, Yahua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOSTWARE: FARUSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4649, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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Best Local Similarity 95.9
Matches 509; Conservative
                                                                                                                                                                                                                    LOCATION: (1)...(643)
OTHER INFORMATION: n = A,
                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
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US-10-042-894A-17
                                                                                                                                      LENGTH: 643
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Sequence 18, Application US/10042894A
Publication No. US20030009011A1
GENERAL INFORMATION:
APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
ITILE OF INVENTION: No. US2003009011A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof

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US-1U-U42-894A-19
; Sequence 19, Application US/10042894A
; Publication No. US2003009011A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Jinrui
APPLICANT: Wang, Hongyu
; APPLICANT: Wang, Hongyu
; APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: OGNES and USES Thereof
; TITLE OF INVENTION: Genes and USES Thereof
; TITLE OF INVENTION: US/10/042,894A
; CURRENT APPLICATION NUMBER: US/10/042,894A
; CURRENT PILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,465
; PRIOR PILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 37
; SQCTWARES FREESE (for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: DAA
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                                                                                                                                                                                                                                                                       285 GGCGCAGCCCGGGAGCCGCATCCTCACCTCGACGACGACGACCTCCTCGCGGGGTTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667 CICAAGGCGTGGTTCGAGGAGCAGACTCTGTTCCACTTCTACTCGGCGTCGATTCTTCTG
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Best Local Similarity 90.2%; Pred. No. 3.1e-44;
Matches 238; Conservative 0; Mismatches 21; Indels 5;
                                                                                                                                  DB 20; Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   525 GGAGGTGAAGGCCATGGACACCGCCGCGCGTCCGCCGCGTGCTCCGGCG
                                                                                                                                                                                                   51; Indels
                                                                                                                                  Score 220.8; DB 2
Pred. No. 1.4e-52;
0; Mismatches 51
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_109799C.1
US-10-425-115-10743
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LOCATION: (1)...(353)
OTHER INFORMATION: n = A, T, C, or G
                                                                                                                              Query Match
Best Local Similarity 82.3%;
Matches 237; Conservative
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| Publication No. US20040214272A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cao, Yongwai;
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With:
| TITLE OF INVENTION: Plants |
| TITLE OF INVENTION: Plants |
| TITLE OF INVENTION: WIMBER: US/10/425,115 |
| CURRENT APPLICATION NUMBER: US/10/425,115 |
| CURRENT FILING DATE: 2003-04-28 |
| SEQ ID NO 10743 |
| LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 IGTTTCTGACATTGTTCCAGAGACTCCTCAGACGCAGCCTTTGGGTCCTTCTTAAGAAAA 301
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LOCATION: (1)..(295)
OTHER INFORMATION: unsure at all n locations
FILE REPERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT APPLICATION NUMBER: US/10/042,894A
PRIOR PILING DATE: 2002-01-09
PRIOR PILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARKE: FASLESE for Windows Version 4.0
SEQ ID NO 18
LENGTH: 519
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                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(519)
; OTHER INFORMATION: n = A, T, C, or G
US-10-042-894A-18
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Best Local Similarity 89.4%;
Matches 328; Conservative
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10-425-115-10743
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Search completed: June 17, 2005, 04:00:54 Job time: 893 secs
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                                                                                                                                                                                                                               RESULT 15
US-10-042-894A-11
i Sequence 11, Application US/10042894A
j Publication No. US20030009011A1
j GENERAL INFORMATION:
i APPLICANT: Bach, Larry
j APPLICANT: Wang, Hongyu
j TITLE OF INVENTION: No. US20030009011A1e1 Inositol Polyphosphate Kinase
j TITLE OF INVENTION: Genes and Uses Thereof
j TITLE OF INVENTION: Genes and Uses Thereof
j TITLE OF INVENTION NUMBER: US/10/042,894A
j CURRENT FILING DATE: 2001-09
j PRIOR APPLICATION NUMBER: US 60/261,465
j PRIOR FILING DATE: 2001-012
j SOFTWARE: FastSEQ for Windows Version 4.0
j SEQ ID NO. 11
librication of the property of 
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                              181 AGCTCTGCTAGCTGATCAAGTTCCGTTTCTTGACATTGTTCCAGANACTCCTTAGACGCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 184.6; DB 14; Length 1195;
Pred. No. 4.2e-42;
0; Mismatches 349; Indels 27;
                                                                                                                                   AGCCTTTGGGTCCTTCTTAAGAGA
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55.6%;
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Matches 471, Conservative
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LOCATION: (116)...(1048)
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CC344833 OGIAQ20TV
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CG44624 OGIAB23TV
CC744864 OGIAB23TV
CC74960 OGIAB23TV
CG284572 OGMFE61TH
CG776236 1123005E0
CA245555 SCGFT106
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CA10695 SCCRT100
AY109355 Zea mays
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CC724950 OGIAB23TH
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CG13495 PUVCG54TD
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Copyright (c) 1993 - 2005 Compugen Ltd.
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9712 Medical Center Drive, Rockville, MD
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
(bas. Panicoideae; Andropogoneae; Zea.
Whitelaw, C.A., Qea.)
Whitelaw, C.A., Deackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Unpublished (2002)
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                                                                                                                                            292 TCCCCCGGTTCCACGGCACGCGACTCCTCCCCACCGAGGCGCAGCCCGGGAGCCGCATC
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TR
Class: sheared ends.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Other GSSs: OGSAD407H
Contact: Cathy Whitelaw
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Class: sheared ends.
Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poalea, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                  1 (bases 1 to 867)
Mitchaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGLAB23TH
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/db.care="caxon:4577"
/clone="zawBwa0307c22"
/clone=lb="zm-0.7 1.5_KB"
/note="Vector: pBGSk-; Site 1: HincII; 0.7-1.5
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al Similarity 89.4%; Pred. No. 8.4e-141;
753; Conservative 0; Mismatches 27;
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/strain="B73"
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/organism="Zea mays"
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Location/Qualifiers
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Email: whitelaw@tigr.org
Seq primer: TF
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  GI:32143893
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/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
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/strain="B73"
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  organism="Zea mays'
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CG284572 119 bp DNA linear GSS 25-AUG-2003 OGWIF61TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0584K02, genomic survey sequence. CG284572 GC384572. GI:34198786 GSS.
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                                                                                               Gaps
                                                                                                 <u>ب</u>
                                                                Length 801
                                                                                                 Indels
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
                                                                Score 620; DB 6; L
Pred. No. 5.7e-135;
0; Mismatches 82;
                                                                    46.1%;
89.2%;
                                                                                                   701, Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA134480 801 bp mRNA linear EST 24-SEP-2003 SCJFRT1061H11.9 RT1 Saccharum officinarum cDNA clone SCJFRT1061H11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RTI"
/note="Organ: Root tips (0.3cm-long) from adult plants;
/note="Organ: Root tips (0.3cm-long) from adult plants;
vector: psport1; Site 1: Salf; Site 2: Not1; An
unidirectional Dibrary generated from [Root tips
(0.3cm-long) from adult plants]. cDNA was prepared from
polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 KD were directionally cloned into the
vector. Details of each source of RNA and library
                                                      625
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 061 row: H column: 11
Seg primer: T7 Promoter Primer.
Location/Qualifiers
                                        ACATTGTCGGCGTCCGCCGCGGGGTCCGGCGTGTCATCGTTGCCGACGAGGGG
                                                                                                      CTTCTGGGCTATGATGCTGCTGCAGTCGCAGCCGGAGATGGGGGTGAGGGTGACGGTG
                                                                                                                                                                                                                                             CTTCTGGGCTATGATGCTGCTGCAGTGGCAGCAGGCGAGGTGGGGGTGGGGTAACAGTG
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                                                                                                                                                                         CGCGAGCTCAAGGCGTGGTTCGAGGGGCAGACTCTGTTCCACTTCTACTCGGCGTCGATT
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                    ACACCGCCGCCGCCGCCGCGCTCCGGCGCTACGTGTCATCCG-TTGCCGACGAGGGG
                                                                                       ATGGACTGTGCGCTCGCCGCGGCGGTGTACGGAGGAAAAGGTGGAGTCTTGTCACAGCTG
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Saccharum officinarum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4547"
/clone="SCJFRT1061H11"
/lab_host="DH10B"
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AUTHORS
TITLE
JOURNAL
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CA134480
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634 615

454 435 514 495 574 555 675

694

754

813

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/clone libs="1123" - RescueMu Grid L"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BgJII;
RescueMu is a 4.9 bb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastace.edu' and follow the links for 'RescueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BgJII, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 29-OCT-2003
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                                                                                                  708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 591)
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GCCGACGAGGAGGATGGACTGCGCGCTCTGCGTGTACGGAGGAAAAGGTGGAGTC
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/cultivar="mixed background W23/A188/B73/K55"
/tissue_type="leaf"
/tissue_type="leaf"
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Fax: 650 725 8221
Email: walbotoestanford.edu
Plate: 1123005 column: 3
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%; Score 589.4; DB 9;
llarity 99.8%; Pred. No. 8.7e-128;
Conservative 0; Mismatches 1;
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organism="Zea mays"
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/lab_host="DH108"
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                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                    Tosses 1 to 719)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Frser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citck,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
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/clone="zxwBMA0584K22"
/clone="bl=zxw 0.7_1.5 KB"
/note="Vector: pBcSK.; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 45.6%; Score 613.2; DB 9; 11 Similarity 90.4%; Pred. No. 2.2e-133; 700; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .719
/organism="Zea mays"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: whitelaw@tigr.org
Seq primer: TR
                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
Other GSSs: OGWIF61TV
Contact: Cathy Whitelaw
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Matches 700; Conserva
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/dlone lib="Saccharum officinarum FLS"
/dlone lib="Saccharum officinarum FLS"
/note="Organ: Developed inflorescence (20cm-long) without rachis; vector: pSport1; Site_1: Sal1; Site_2: Not1; An unidirectional cDNA library generated from Tbeveloped inflorescence (20cm-long) without rachis]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invircogen): The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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RT1 Saccharum officinarum cDNA clone SCCCRT1004G05
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                                                                                                                                                                                                                                                                                                                                                                                                 37 CCCCTTCCCCATACCATGTCCGACCTCCACCGGCGGAGCACCAAGTCGCCGGCCACCGC
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larity 93.7%; Pred. No. 6e-122;
Conservative 0; Mismatches 39;
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5', mRNA sequence.
CA130685
CA130685.1 GI:3501
EST.
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es 599; Conserv
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA245555 656 bp mRNA linear EST 25-SEP-2003 SCEGFL5081A03.g Saccharum officinarum FL5 Saccharum officinarum cDNA clone SCEGFL5081A03 5', mRNA sequence.
           GCCGGCCACCGCCTCCGCCAGCAAGCTGGGCCCCCTCTACGACGGCTCCAGCCCCGGCCTCTTC 120
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1139
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
                                                                                                TACAAGCCGCTCCAGGCCGGCGACCGTGGGGAGCACCACGCTTCTATGAGGCGTTC
                                                                                                                                                                                  TCGCCCACGCCGCCGTCCCGGCCCCCACCACCTTCTTCCCCCCGGTTCCACGGC
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Vettore, A. L., da Silva, F. R., Kemper, B. L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P

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    /organism="Saccharum officinarum"

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Plate: 081 row: A column: 03
Seg primer: T7 Promoter Primer.
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/db_xref="taxon:4547"
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Submitted (15-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.igr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTC 17-0CT-2002
375 TCGCCGGAGCCCTACGTCGCCAAGTGCCTCGCCAAGGACCGCGGGACCACGAGCATTCTG 434
                                                                                                                                                                           517 GAGGGCCCGGAGGTGAAGGCCATGGACACCGCCGGCGTCCGCCGCGCGTGCTCCGGCGCTAC 576
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                            CTCGGATTCCGCGTCTCCGGCGTCCGAGTCGTCGGCCCCCGAGGGCGCCCGTGTGGCGGACG
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                                                                                             435 CTCGGATTCCGCGTCTCCGGCGTCGTCGGTCCCGAGGGCGCCGTGTGGCGGACT
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
(bases 1 to 3374)
                                                                                                                                                                                                                                                                                                                                                                                                               636 AAAAGGTGGAGTCTTGTCACAGCTGCGCGAGCTCAAGGCGTGGTTCGAGGAGCAGACTCT
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67.7%; Pred. No. 2.8e-120;
ive 0; Mismatches 259;
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/db_xref="MaizeDB:632179"
/db_xref="taxon:4577"
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//olone libe "RI"
//octor: psporti; Site is Site 2: Not I; An
unidirectional cDNA library generated from [Root tips
unidirectional cDNA library generated from [Root tips
(0.3cm-long) from adult plants]. cDNA was prepared from
polyth mRNA using SuperScript Plasamid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
                                                                                       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                              Saccharum officinarum
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Centroo de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 004 row: G column: 05
Seg primer: T7 Promoter Primer.
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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//mol rype="mRNA"
/db xref="earch-4547"
/clone="SCCCRT1004G05"
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CA202412 671 bp mRNA linear EST 25-SEP-2003 SCRLFL1009H02.g FL1 Saccharum officinarum cDNA clone SCRLFL1009H02

RESULT 12 CA202412 LOCUS DEFINITION

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/ncce="Organ: Inflorescence at begining of development (1cm-long); Vector: pSport1; Site 1: Sal1; Site 2: Not1; An unidirectional cDNA library generated from Indirectional cDNA library generated from [Inflorescence at begining of development (1cm-long)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand CDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                     Contact: Arruda P
Contact: Arruda P
Contact: Arruda P
Contro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1189
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.uneap.br
http://www.bcccenter.fcav.uneap.br
Plate: 009 row: H column: 02
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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/mol_type="mRNA"
/mol_type="mRNA"
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/lab_host="DH108"
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/clone_lib="FL1
5', mRNA sequence.
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1 (bases 1 to 722)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Cinsortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGLAB23TV
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                                      TCACAGCTGCGCGAGCTCAAGGCGTGGTTCGAGGAGCAGACTCTGTTCCACTTCTACTCG 711
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TCCGGCGTCCGGGTCGTCCCGAGGGCGCCGTGTGGCGGACTGAGCGCCCCGGAGGTG 361
                                                                          GACGAGGGGATGGGCTCGCCCCCGCGCGCGTGTACGGAGAAAGGTGGAGTCTTG 651
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/clone lib="zm 0.7 1.5 KB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 40.2%; Score 540.8; DB 9; Length 722; Il Similarity 89.6%; Pred. No. 2.4e-116; 638; Conservative 0; Mismatches 17; Indels 57
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Tel: 301-838-5843
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Class: sheared ends.
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Clade; Panicoddeae; Andropogoneae; Zea.
E 1 (bases 1 to 593)
S Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Karzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Cancarn, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Conteat: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Fax: 516 367 8884
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TCCTCACCTCGTCCTCGACGACCTCCTCGCGGGGTTTCAGGCGCCCTGCGTCGCAGACAT
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GI:35013916
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88.6%;
                                                 Saccharum officinarum
                                                                  Saccharum officinarum
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Best Local Similarity
Matches 592; Conserv
              CA130686.1
                                                                                                                                     complex.
 CA130686
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AUTHORS
TITLE
JOURNAL
COMMENT
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                  ORGANISM
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                                                                                                                                                                                                     /clone_lib="WGS-ZmaysF (DHSa methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
/note="Crgan: immature ears; Site_1 = xba I; Site_2: Xba I;
/note="Crgan: degreted with XbaI and one nucleoFide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between O.8 and 3 kb and were cloned into the vector (:x/y
reads in Milmply. .b/g reads in pUC19). The same ligation
was transformed into DHSa."
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                                                                                                                                                                                                                                                                                                                                                                                              39.9%; Score 535.6; DB 8; Length 593; 97.9%; Pred. No. 3.9e-115;
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                    1. .593
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                 Class: shotgun
High quality sequence stop: 593.
Location/Qualifiers
Place: 1151 row: a column: 11
Seg primer: -21M13UnivFwd
                                                                                                                                                     db_xref="taxon:4577"
                                                                                                                                                                       /clone="ii51a11"
/lab_host="DH5a"
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 97.9
Matches 564; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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Vector: pSport1; Site 1: Sal1; Site 2: Not1; An
unidirectional CDNA library generated from (Root tips
(0.3cm-long) from adult plants]. cDNA was prepared from
poly4-mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.uneap.br
Plate: 004 row: G coluum: 06
Seg primer: T7 Promoter Primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 and Arruda, P
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Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 525.6; DB 6; Length
Pred. No. 9e-113;
0; Mismatches 74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Universidade Estadual de Campinas
Caixa Poetal 6010, 13083-970, Campinas SP,
TS 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .744
//organisma="Saccharum officinarum"
//mol_type="mRNA"
/db_xref="taxon:4547"
                                                                                                                                                                                                                                                                                           Vettore, A.L., da Silva, F.R., Kemper, E.L.
The libraries that made SUCEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="SCCCRT1004G06"
/lab_host="DH10B"
/clone_lib="RT1"
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CA130686 SCCRT1004G06.g RT1 Saccharum officinarum cDNA clone SCCCRT1004G065., mRNA sequence.

97 TCGCCGGAGCCCTACATCGCCAAGTGCCTCGCCAAGGACCGCGGGACCACGAGCGTTCTG 456	57 CTCGGATTCCGCGTCCCGGGGTCCGGCCCCCGAGGGCCCGTGTGGCGGACG 516		77         GTGTCATCCGTTGCCGACGAGGGATGGACTGTGCGCTCGCCGCGGGGGGTGTACGGAGGA         6.36           1	37 AAAGGTGGAGTCTTGTCACAGCTGCGGGAGGTCAAGGCGTGGTTCGAGGAGCAGTCTG 696 	77 TTCCACTT 704 
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Search completed: June 17, 2005, 01:52:45 Job time: 4778 secs

Sequence 177, App Sequence 182, App Sequence 7871, Ap Sequence 788, Appli Sequence 6598, Ap Sequence 6598, Ap Sequence 6598, Ap Sequence 6519, Ap Sequence 6519, Ap Sequence 1190, Ap Sequence 1190, Ap Sequence 7, Appli Sequence 7, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli

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Sequence:

Searched:

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99 CICCGCCAGCAAGCIGGGCCCGCICAICGACGCCICCGGCCTCTICIACAAGCCGCTCCA 158
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Barent No. 641702

GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905

CURRENT PAPLICATION NUMBER: US/09/249,585A

CURRENT PILING DATE: 1999-02-11

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 1926
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Pred. No. 7.8e-07;
0; Mismatches 294; Indels
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US-09-902-540-788
US-09-372-42A-9
US-09-252-991A-6598
US-09-252-991A-6578
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US-09-902-540-130
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US-09-902-540-130
US-09-9128-155-16
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OTHER INFORMATION: template strand of EBNA-1 DNA
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Best Local Similarity 45.6%;
Matches 246; Conservative
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ORGANISM: Epstein Barr Virus
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LOCATION: (1)..(1926)
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Sequence 5, Appli
Sequence 1318, Ap
Sequence 1154, Ap
Sequence 1147, Ap
Sequence 1147, Ap
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Sequence 881, App
Sequence 1, Appli
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Sequence 13679, A
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Sequence 1, Ap
Sequence 19, A
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Sequence 3,
Sequence 2
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                                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-902-540-1154

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Listing first 45 summaries
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                                                                                    APPLICANT: ASSHERY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MODANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REPERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58.6; DB 3; Length 38506;
Pred. No. 0.00087;
0; Mismatches 274; Indels 0;
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EARLIER APPLICATION NUMBER: CIP OF 09/141,908

EARLIER APPLICATION NUMBER: CIP OF 09/141,908

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1999-05-06

EARLIER FILING DATE: 1999-02-08

EARLIER FILING DATE: 1999-02-08

EARLIER APPLICATION NUMBER: 60/119,139

EARLIER APPLICATION NUMBER: 60/109,800

EARLIER APPLICATION NUMBER: 60/100,800

EARLIER APPLICATION NUMBER: 60/100,800

EARLIER APPLICATION NUMBER: 60/009,000

EARLIER FILING DATE: 1998-09-22

EARLIER FILING DATE: 1998-05-28

WUMBER OF SEQ IN ONS: 34
Sequence 19, Application US/09320878A Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-19
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Matches 223; Conservative
                                Patent No. 6117659
GENERAL INFORMATION:
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RESULT 6
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
22631 CGCGGCCGACGGCCTCG 22647
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                                                                                                                                                                  RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 CTTCCCCCCGGTTCCACGGCACGCGACTCCTCCCCACCGAGGCGCAGCCCGGGGAGCCGCA 305
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                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/09141908
; Patent No. 6503741
; GENERAL INFORMATION:
    APPLICANT: BETLACH, Melanie C.
    APPLICANT: BETLACH, Mary
; APPLICANT: BETLACH, Mary
; APPLICANT: BETLACH, Mary
; APPLICANT: AND SETLACH, Mary
; APPLICANT: TANG, Li
; TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
; TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
; TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
; FILE REFERENCE: 300622002100
; CURRENT APPLICATION NUMBER: US/09/141,908
; EARLIER PILING DATE: 1998-06-26
; EARLIER FILING DATE: 1997-04-30
; EARLIER FILING DATE: 1997-04-30
; EARLIER FILING DATE: 1998-03-05
; EARLIER FILING DATE: 1998-03-05
; EARLIER FILING DATE: 1998-05-28
; WUMBER OF SEQ ID NOS: 31
; GARLIER FILING DATE: 1998-05-28
; WUMBER OF SEQ ID NOS: 31
; GARLIER FILING DATE: 1998-05-28
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Pred. No. 0.00087;
0; Mismatches 274; Indels 0;
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Best Local Similarity 44.9%;
Matches 223; Conservative
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SEQ ID NO 1
LENGTH: 38506
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22391 GGGCCGGTTCGTCCTCGACCTCGGGGAAGCCCCGGACGCCCGGACGCACCCC 22450
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                                                                                                                                                                                                 Length 38506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.4%; Score 58.6; DB 4;
44.9%; Pred. No. 0.00087;
tive 0; Mismatches 274;
; Sequence 19, Application US/09657440; Patent No. 6509455; GENERAL INFORMATION: APPLICANT: ASHLEY, Gary APPLICANT: BETLACH, Melanie C.; APPLICANT: BETLACH, Mary C.; APPLICANT: TANG, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Streptomyces venezuelae
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Matches 223; Conservative
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Sequence 13679, Application US/09949016

Fatent No. 6812339
GENERAL INFORMATION
J GENERAL INFORMATION
FAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE OF INVENTION NUMBER: 05/241,755
CURRENT FILING DATE: 2000-10-20
FRIOR PELLOR OF SECTION NUMBER: 66/237,768
FRIOR APPLICATION NUMBER: 66/237,768
FRIOR PELLOR DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
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46.2%; Pred. No. 0.00076;
cive 0; Mismatches 226; Indels
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3%;
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Best Local Similarity
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US-09-949-016-13679/c
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; ORGANISM: Human
US-09-949-016-13686
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; ORGANISM: Human
US-09-949-016-13679
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Sequence 13686, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
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                                                                                                                                                                                                                                                          APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
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4.4%; Score 58.6; DB 3; Length 4411529;
Best Local Similarity 44.4%; Pred. No. 0.0042;
Matches 235; Conservative 0; Mismatches 294; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                       WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-949-016-13686/c
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LENGTH: 4411529
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48.2%; Pred. No. 0.00042;
iive 0; Mismatches 175;
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxcocccus xanthus Genom:
FILE REFERENCE: 38-10(15449)B
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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US-09-902-540-7284
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Batent No. 6632930

GREREAL INFORMATION:
APPLICANT: HOWARD, JOHN
APPLICANT: HOMARD, JOHN
APPLICANT: MACHELE
APPLICANT: WANG, HUAMING
APPLICANT: HUAMING
APPLICANT: WANG, HUAMING
APPLICANT: WANG, HUAMING
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Local Similarity 46.2%; Pred. No. 0.00037;
nes 230; Conservative 0; Mismatches 265; Indels
                          0; Mismatches 226; Indels
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                                                                                                                                                              Sequence 687, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: 02/01-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

WUMBER OF SEQ ID NOS: 16825
1314 CCGGGTGGTGAAGGCGGACCAGCTGTCGGACCGCGCTTCTTCTACCGGTCGGACCAGTT 1373
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Pred. No. 0.00061;
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                                       582 ATCCGTTGCCGACGAGGGGATGGACTGTGCGCTCGCCG
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Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Abou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Abundi, Vinod
APPLICANT: Shang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Mang, Jian-Rui
APPLICANT: Mang, Jian-Rui
APPLICANT: Mang, Jian-Rui
APPLICANT: Mang, Vinqing
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Matches 163; Conservative
                                                                                                                                RESULT 11
US-09-902-540-687/c
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US-09-799-451-881
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46.7%; Pred. No. 0.00074;
iive 0; Mismatches 209; Indels 0
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APPLICANT: Khosla, Chaitan
TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
FILE REFERENCE: 28600-20210.00
CURRENT APPLICATION NUMBER: US 80/9/773,816
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-01-31
                                                                                          APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6/83966el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
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                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SEQ ID NO 881
LENGTH: 4530
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Yamazaki, Victoria
Chen, Rui-hong
Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 46.7
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (330)..(4265)
US-09-799-451-881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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CGACGGCTCCTCCTTCTACAAGCCGCTCCAGGCCGCGACCGTGGGGAGCACGAGGT 185
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LENGTH: 36778
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                                                                                                                                                                                                                                                                          311 ACCTCGTCCTCGACGACCTCCTCGCGGGGTTTCAGGCGCCCTGCGTCGCACATCAAGA 370
                                                                                                                                                                                                                                                                                                                                               371 TCGGCCCCATCACGTGGCCACCGAGTTCGCCGGAGCCCTACATCGCCAAGTGCCTCGCCA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 GCCCCGAGGGCGCCGTGTGGCGGACGGAGCGCCCGGAGGTGAAGGCCATGGACACCGCCG 550
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Pred. No. 0.0014;
                                                                                                                                                                                                        Score 57.6; DB 3; Length 2 Pred. No. 0.0013; 0; Mismatches 184; Indels
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Patent No. 6265202

GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H. H.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
APPLICANT: Liu, W.
TITLE OF INVENTION: DNA encoding methymycin and pik
TITLE PREFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26

CURRENT FILING DATE: 1998-06-26

CURRENT FILING DATE: 1998-06-26

SOFTWARE: FREQ for Windows Version 3.0

SEQ ID NO 32
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                               ) OTHER INFORMATION: n = A,T,C or G
US-09-773-816-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.2%;
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Best Local Similarity 49.2%;
Matches 181; Conservative
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Matches 222; Conservative
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New inositol polyphosphate kinase polynucleotides and polypeptides, useful in modulating phytic acid biosynthesis by decreasing phytate increasing the nutritional value animal feed.
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polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with altered phenotype. IPPR proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The
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/product= "Maize IPPK protein
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P-PSDB; AAE26195.
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                                            The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymuclectides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Onlymucleorides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The
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                                                                                                                                                                                                         Length 922;
                                                                                                                                                                               Sequence 922 BP; 137 A; 327 C; 288 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                       Score 864.4; DB 6;
Pred. No. 4.2e-171;
                                                                                                                                                                                                                                   0; Mismatches
                        Claim 1; Page 62-63; 86pp; English
                                                                                                                                                     present sequence is maize IPPK DNA
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ilarity 98.8%;
Conservative (
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Best Local Similarity
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Bolynucleorides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            phytic acid;
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nutritional value; animal feed; transgenic; gene; ds
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                                                                                            TCCAGAGACTCCTCAGACGCAGCCTTTGGGTCCTTCTTAA
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Pred. No. 5.5e-167;
0; Mismatches 22;
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                                                          TCCGGAGACTCCTCATACGCAGCCTTT
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84. .806
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97.2%;
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Matches 890; Conservative
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llarity 97.5%; Pred. No. 1.9e-165;
Conservative 0; Mismatches 21;
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                                                                     "Maize IPPK
Location/Qualifiers
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P-PSDB; AAE26194.
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phytic acid;

DNA #2

Maize inositol polyphosphate kinase (IPPK)

Maize; enzyme; inositol polyphosphate kinase; IPPK; i nutritional value; animal feed; transgenic; gene; ds

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                                                                                                                                                               837 T; 0 U; 0 Other;
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                                                                                                                                                                                           Score 740.4; DB 6;
Pred. No. 4.4e-145;
0; Mismatches 31;
                                                                                                                                                                C; 856 G;
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90.2%;
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Matches 862; Conservative
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Pred. No. 8.4e-134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.0%; Score 470.4; DB 6; Length 95.9%; Pred. No. 9.5e-89; ive 0; Mismatches 18; Indels
                                                                                                                                        Cahoon RE;
                                                                                                                                        Rafalski JA,
                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is maize IPPK DNA
                                                                                                                                                                                                                                                                      Claim 1; Page 74; 86pp; English.
                                                                                                             (PION-) PIONEER HI-BRED INT INC
                                                      09-JAN-2002; 2002WO-US003120
                                                                                 12-JAN-2001; 2001US-0261465P
                                                                                                                                         Wang H,
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Best Local Similarity
Matches 509; Conserva
                                                                                                                                                                  WPI; 2002-636540/68.
                                                                                                                                         Beach LR,
WO200259324-A2
                                                                                                                                                                                                                                            animal feed.
                          01-AUG-2002
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and rahising anti-idiotypic antibodies. The present sequence is maize IPPK DNA
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                                                                                                                                                                             Maize; enzyme; inositol polyphosphate kinase; IPPK; phytic acid;
nutritional value; animal feed; transgenic; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.2%; Score 298.4; DB 6;
89.4%; Pred. No. 8.5e-53;
tive 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cahoon
                                                                                                                                        Maize inositol polyphosphate kinase (IPPK) DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 75; 86pp; English.
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519
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Best Local Similarity 89.4°
Matches 328; Conservative
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DNA;
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  standard;
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and ralising anti-idiotypic antibodies. The present sequence is Eucalyptus grandis IPPK DNA
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GGCTCTGCTCGCTGATCAAGTTC--GTTTCTGACATTGTTCCGGAGACTCCTCATACG-C 901
                       181 AGCTCTGCTAGCTGATCAAGTTCCTTGACATTGTTCCAGANACTCCTTAGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 GCCCGCTCATCGACGCTCCTCTACAAGCCGCTCCAGGCCGCGACCGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 CCGACCTCCACCCGCCGGAGCACCAAGTCGCCGGCCACCGCGCCTCCGCCAAGCTGG
                                                                                                                                                                                                                                                                                                                                                         sitol polyphosphate kinase; IPPK; phytic acid; transgenic; value; animal feed; gene; ds.
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                                                                                                                                                                                                                                                                                                                      Eucalyptus grandis inositol polyphosphate kinase (IPPK) DNA
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/*tag= a
/product= "E. grandis IPPK protein"
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Pred. No. 6e-29;
0; Mismatches 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beach LR, Wang H, Rafalski JA,
                                                                          902 AGCCTTTGGGTCCTTCTTAAGAGA 925
                                                                                                             241 AGCCTTTGGGTCCTTCCTTAAAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Local Similarity 55.6%;
les 471; Conservative
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                                                                                                                                                                                                                                                                                                                                                           ne; inositol polyphosphate kinase; IPPK; phytic acid; value; animal feed; transgenic; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RE;
                                                                                                                                                                                                                                                                                                                        Maize inositol polyphosphate kinase (IPPK) DNA #8
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Pred. No. 1.7e-30;
0; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rafalski JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is maize IPPK DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 75; 86pp; English
                                                                                                                                                                                                        AAD43521 standard; DNA; 353 BP.
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polymucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The present sequence is soybean IPPK DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCATGGACACCGCCGCGGCGCGCGCGCGCGCCT---ACGTGTCATCCGTTGCC 591
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0; Mismatches 340;
protein"
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/product= "Soybean IPPK
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                                                                                        603 GAGCGCTTGCAGAAGCTCAAGGACTGGAGGTTCAGACGGTGTATCACTTCTATTCT
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nutritional value, animal feed; gene, ds.
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modulate their activity and raising anti-idiotypic antibodies. present sequence is P. argentatum IPPK DNA
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Pred. No. 1.1e-21;
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23-AUG-1999;
23-AUG-1999;
Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 23077
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9905-0123180P

9905-012548P

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                       (first entry)
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                      17-OCT-2000
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        AAC39023;
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CAGCCCGGGGAGCCGCATCCTCACCTCGTCCTCGACGACCTCCTCGCGGGGTTTCAGGCG 348
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Best Local Similarity 53.0%;
Matches 453; Conservative
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway;
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             GGAAAAGGTGGAGTCTTGTCACAGCTGCGGGGGCTCAAGGCGTGGTTCGAGGAGCAGACT
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99US-0161361P.
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